STIC Search Report
Biotech-Chem Library

USPTO

TO: Ruixiang Li
Location: rem/4D59/4C70
Art Unit: 1646
Wednesday, May 31, 2006
Case Serial Number: 10/619992

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian (ASRC Aerospace)
STIC Biotech/Chem Library
(571)272-4161

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78733   *190795*   *M2*

From:	Li, Ruixiang
Sent:	Tuesday, May 23, 2006 9:19 AM
To:	STIC-Biotech/ChemLib
Subject:	Sequence search of Application No.10/619,992

Please do a standard search on:

SEQ ID NO: 2 against interference amino acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D59
Mail Box 4C70
(571) 272-0875

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

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OM protein - protein search, using sw model

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Run on: May 24, 2006, 12:48:33 ; Search time 35 Seconds
               2978.542 Million cell updates/sec
               (without alignments)

Title: US-10-619-992-2
Perfect score: 6215
Sequence: 1 MPVQAAQWTEFLSCPICYNE.........MSEDKNDFLKPVANGKMVNS 1191

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 8753062B residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents_AA:*
  1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
  2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
  3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
  4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
  5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
  6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
  7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	6215	100.0	1191	2	US-10-619-992-2	Sequence 2, Appli
2	6207	99.9	1191	2	US-09-921-099A-2	Sequence 4, Appli
3	843	13.6	1048	2	US-09-921-099A-11	Sequence 11, Appli
4	611	9.8	522	2	US-10-047-3665	Sequence 3665, Ap
5	194	3.1	2185	2	US-09-854-856-36	Sequence 36, Appl
6	194	3.1	2185	2	US-10-010-720-36	Sequence 36, Appl
7	194	3.1	2245	2	US-09-854-856-4	Sequence 4, Appl
8	194	3.1	2245	2	US-10-010-720-4	Sequence 4, Appl
9	194	3.1	2322	2	US-09-854-856-34	Sequence 34, Appl
10	194	3.1	2322	2	US-10-010-720-34	Sequence 34, Appl
11	194	3.1	2382	2	US-09-854-856-2	Sequence 2, Appli
12	194	3.1	2382	2	US-10-010-720-2	Sequence 2, Appli
13	193.5	3.1	1939	2	US-09-854-856-48	Sequence 48, Appl
14	193.5	3.1	1939	2	US-10-010-720-48	Sequence 48, Appl
15	193.5	3.1	1999	2	US-09-854-856-16	Sequence 16, Appl
16	193.5	3.1	1999	2	US-10-010-720-16	Sequence 16, Appl
17	193.5	3.1	2076	2	US-09-854-856-46	Sequence 46, Appl
18	193.5	3.1	2136	2	US-10-010-720-46	Sequence 46, Appl
19	193.5	3.1	2136	2	US-09-854-856-14	Sequence 14, Appl
20	193.5	3.1	2136	2	US-10-010-720-14	Sequence 14, Appl
21	193	3.1	1911	2	US-10-010-720-64	Sequence 64, Appl
22	193	3.1	1911	2	US-09-854-856-64	Sequence 64, Appl
23	193	3.1	1971	2	US-09-854-856-32	Sequence 32, Appl
24	193	3.1	1971	2	US-10-010-720-32	Sequence 32, Appl
25	193	3.1	2048	2	US-09-854-856-62	Sequence 62, Appl
26	193	3.1	2048	2	US-09-854-856-26	Sequence 62, Appl
27	193	3.1	2108	2	US-09-854-856-30	Sequence 30, Appl
28	193	3.1	2108	2	US-10-010-720-30	Sequence 30, Appl
29	193	3.1	2179	2	US-09-949-016-8129	Sequence 8129, Ap
30	189	3.0	1323	2	US-09-248-796A-19543	Sequence 19543, A
31	188	3.0	827	2	US-09-248-796A-17307	Sequence 17307, A
32	187	3.0	2157	2	US-09-854-856-52	Sequence 52, Appl
33	187	3.0	2157	2	US-10-010-720-52	Sequence 52, Appl
34	187	3.0	2217	2	US-09-854-856-20	Sequence 20, Appl
35	187	3.0	2217	2	US-10-010-720-20	Sequence 20, Appl
36	187	3.0	2294	2	US-09-854-856-50	Sequence 50, Appl
37	187	3.0	2294	2	US-10-010-720-50	Sequence 50, Appl
38	187	3.0	2354	2	US-09-854-856-18	Sequence 18, Appl
39	187	3.0	2354	2	US-10-010-720-18	Sequence 18, Appl
40	182.5	2.9	4019	2	US-10-133-425	Sequence 425, App
41	182	2.9	2004	2	US-09-854-856-58	Sequence 58, Appl
42	182	2.9	2004	2	US-10-010-720-58	Sequence 58, Appl
43	182	2.9	2032	2	US-09-854-856-42	Sequence 42, Appl
44	182	2.9	2032	2	US-10-010-720-42	Sequence 42, Appl
45	182	2.9	2064	2	US-09-854-856-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-921-099A-2
; Sequence 2, Application US/09921099A
; Patent No. 6602707
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene ar
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/09/921,099A
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-921-099A-2

Query Match 100.0%; Score 6215; DB 2; Length 1191;
Best Local Similarity 100.0%;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTD 60

Qy   61 IDVLPVNFALLQLVGAQVPDHQSIKLSNIGENKHYEVAKKCVEDLALYLYKPLSGGKGVAS 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 IDVLPVNFALLQLVGAQVPDHQSIKLSNIGENKHYEVAKKCVEDLALYLYKPLSGGKGVAS 120

Qy 121 LNQSALSRPMQRKLVTLLVNCQLVEBEGRVRAMRAARSLGERTVTELILQHQNPQOLSANL 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 LNQSALSRPMQRKLVTLLVNCQLVEBEGRVRAMRAARSLGERTVTELILQHQNPQOLSANL 180

Qy 181 WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240

Qy 241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300

Qy 301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360

```
RESULT 2
US-09-921-099A-4
Sequence 4, Application US/09921099A
Patent No. 6602707

GENERAL INFORMATION:

APPLICANT: Hefeneider, Steven
APPLICANT: Merkins, Louise
APPLICANT: Bennett, Robert
APPLICANT: Seiss, Donald
TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene a
FILE REFERENCE: 00-617-A
CURRENT APPLICATION NUMBER: US/09/921,099A
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
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; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-921-099A-4

Query Match             99.9%;  Score 6207;  DB 2;  Length 1191;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 1190;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy     61  IDVLPVNFALLQLVGAQYPEDHQSIKLSNIGENKHYEVAKKCVEDLALYLKPLSGGKGVAS  120
Db     61  IDVLPVNFALLQLVGAQYPEDHQSIKLSNIGENKHYEVAKKCVEDLALYLKPLSGGKGVAS  120

Qy    121  LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANL  180
Db    121  LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANL  180

Qy    181  WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLERPFPQASKTSIG  240
Db    181  WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLERPFPQASKTSIG  240

Qy    241  HVQLLYRASCFKYTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW  300
Db    241  HVQLLYRASCFKYTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW  300

Qy    301  SSLIYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGPDPANLNRLRPHLELLANI  360
Db    301  SSLIYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGPDPANLNRLRPHLELLANI  360

Qy    361  DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLR  420
Db    361  DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLR  420

Qy    421  QQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTPFLLNKVGVNNTVTTTAGNVISVI  480
Db    421  QQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTPFLLNKVGVNNTVTTTAGNVISVI  480

Qy    481  GSTETTGKIVPSTNGISNAENSVSQLLISRSTDSTLRALETVKKVGKVGANGQNAAGPSAD  540
Db    481  GSTETTGKIVPSTNGISNAENSVSQLLISRSTDSTLRALETVKKVGKVGANGQNAAGPSAD  540

Qy    541  SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPPHSENIQYFQ  600
Db    541  SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPPHSENIQYFQ  600

Qy    601  DPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST  660
Db    601  DPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST  660

Qy    661  FSPRDRMNSSPYQPPPQPYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM  720
Db    661  FSPRDRMNSSPYQPPPQPYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM  720

Qy    721  DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD  780
Db    721  DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD  780

Qy    781  QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS  840
Db    781  QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS  840

Qy    841  CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP  900
Db    841  CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP  900

Qy    901  IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSRWSSYGNEATS  960
Db    901  IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSRWSSYGNEATS  960
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```
Qy  961 SAHYVERDRFIVTDLLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE 1020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 SAHYVERDRFIVTDLLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE 1020

Qy 1021 GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL 1080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL 1080

Qy 1081 DIQLGISSQNDQLLNGMAVENGHPVQQHQKEPPRQKQSLGEDHVILEEQKITLLPVTSCF 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 DIQLGISSQNDQLLNGMAVENGHPVQQHQKEPPRQKQSLGEDHVILEEQKITLLPVTSCF 1140

Qy 1141 SQPLPVSISNASCLPITTSVSAGNLILLKTHVMSEDKNDFLKPVANGKWVNS 1191
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 SQPLPVSISNASCLPITTSVSAGNLILLKTHVMSEDKNDFLKPVANGKWVNS 1191
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RESULT 3
US-09-921-099A-11
Sequence 11, Application US/0921099A
Patent No. 6602707
GENERAL INFORMATION:
;   APPLICANT: Hefeneider, Steven
;   APPLICANT: Merkins, Louise
;   APPLICANT: Bennett, Robert
;   APPLICANT: Seiss, Donald
;   TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene a
;   FILE REFERENCE: 00-617-A
;   CURRENT APPLICATION NUMBER: US/09/921,099A
;   CURRENT FILING DATE: 2001-08-01
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: Patentin version 3.0
;   SEQ ID NO 11
;   LENGTH: 1048
;   TYPE: PRT
;   ORGANISM: Caenorhabditis elegans
US-09-921-099A-11

Query Match   13.6%; Score 843; DB 2; Length 1048;
Best Local Similarity   30.6%; Pred. No. 4.3e-59;
Matches 238; Conservative 99; Mismatches 278; Indels 162; Gaps 23;

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Qy   4 QAAQWTEFLSCPICYNEFDENAVHKPISLGCSHTVCKTCLNKLHR--KACPFDQTAINTDI 61
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Db   6 QGGQWQEVLCCSICNRHFNE-TFLPVSLICGHVICRKCAEKPENQTKPCPHDDWKTHHSP 64

Qy  62 DVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVASL 121
        | ||| |||| | :          ||||:  || | :    :||: : |      |  :|
Db  65 SEYPNNVALLSVI--FPRKQCMTLSGAVSEAEKVDQLSIQ-IAKFPEADSERG-GTV 119

Qy 122 NQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILCHQNPQQLSANLW 181
        : : :||:|| |||:|:: ||  : ||::: |  |||||||:||:||   : : |  ||
Db 120 SSREISRTLQRKVLALLCYQWREVDGRLKTLKMCRGISERVMIEIILSIQSNTHVSSQLW 179

Qy 182 AAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVWQRLEPRFPQASKTSIGH 241
         |||||||||||||| :: :|:|:|  |:|   : ||::|::| || :  | |||  :||
Db 180 SAVRARGCQFLGPAMQDDVLRLILMTLETGECTARKNIVMYVVQTLASDYPQVSKTCVGH 239

Qy 242 VVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWS 301
        ||||||||||:|: |||  |||||||||| :| |||||| ||||:|| | |||| :|||
Db 240 VVQLLYRASCFNVLKRDGESSLMQLKEEFRTYESLRREHDSQIVQIAFESGLRIGPDQWS 299

Qy 302 SLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGPDAN---------LNRLRP 352
        :|||   :::|||||||||||| :|   |||||  :| |  |            ||:|||
Db 300 ALLYADQSHRSHMQSIIDKLQSKNSYQQGVEELRAL--AGSQTSMLVPAYRYFLTQVIP 356

Qy 353 HLELLANIDPNPDAVSPTWEQLENAMAVAVKTVVHGLVDFIQNY---SRKGHETPQPQPNS 409
         | :: | : :  :| | :: : :  ::   : | : | ::       |: |::||| :|
Db 357 CLEFFAGTEHEDTSMRMIGDALHQIRILLK--LHCSQODLRKMPKEERRGVILQAEVPGG 414

Qy 410 KYKTSMCRDLRQQGCPRGTNCTFAHSQEELEXYRLRNKKINATVRTPPLLNKVGVNNTV 469
                                      : |
Db 415 --------------GAEAGRI-------MGGGPGGSG 430
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RESULT 4
US-10-104-047-3665
Sequence 3665, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
;   APPLICANT: HELIX RESEARCH INSTITUTE
;   TITLE OF INVENTION: H1-A0105
;   FILE REFERENCE: 6943241e1 full length cDNA
;   CURRENT APPLICATION NUMBER: US/10/104,047
;   CURRENT FILING DATE: 2002-03-25
;   PRIOR APPLICATION NUMBER:
;   PRIOR FILING DATE:
;   NUMBER OF SEQ ID NOS: 4096
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 3665
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-104-047-3665

Query Match   9.8%; Score 611; DB 2; Length 522;
Best Local Similarity   34.1%; Pred. No. 1e-40;
Matches 187; Conservative 76; Mismatches 187; Indels 98; Gaps 27;

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Qy 470 TTTAGNVISVIGTSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGA 529
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Db 431 ------------GGLHPLYSQIDETGRSISRTNPKDNSHNSPQ----------------- 461

Qy 530 NGQNAAGPSADSVTENKICGSPPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVY 589
                                   |||| | : |   | :     :||    :  || :|
Db 462 ----------------------------TPPKQPROKRYQMGIPPNRMG-----YSSDAPFIPSHQQQ 497

Qy 590 PPHSENIQYFQDPRTQIPFEVPQYFPQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPP 649
        ||                  :::   |     |  |  | |               :
Db 498 PPP---QFFNS--QHLPQRFRGRQRGAPPPPPQP-----MPMLIGYD-----MPG 539

Qy 650 ASMPYADHYSTFSPRDRMNSSP-------YQPPPPQPYGPVPPVPSGMYAPVYDSRRIWRPP 704
         :||  |  :    ||  ::         |:||| | | | || |:| :|  | |  || |
Db 540 APMMQATEVLT-ADGQMVNGTPQRVVIMQSPTHLPGGPVVMIPQQQOMVPPPQSMTPVGGP 598

Qy 705 MYQRDDIIRSNSLPPMDVMHSSV-YQTSLRERYNSLDGYYSV---ACQPSEPRTTV 757
        | :    |     ||  : :|       :|  || |        |  |  |  :
Db 599 M-----------GPMGPMTPSIPVQVPNTMWTATSPTCGSVIYPAASPPGQPPHTI 643
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Qy 618 YYPPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYSTFSPRDRMNSSPYQPPP 677
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Db   6 YYTPPP-------------QCVSRFVR----PPPSAPEPAPPYLDHYPPVL-QERVVNSQYGTQPQ 49

Qy 678 QPYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSV--YQTSLRER 735
        |   | |    :| | : | |||   | |: : :  :|  | | ::||    |   |:||
Db  50 Q----YPPI----YPSHYDGRRVVPAPSYTTREEIFRESPI-PIEIPPAAVPSYVPESRER 100

Qy 736 YNSLDGYISVACQP-----PS----EPRTTVPLPREPCGHLKTSCEEQIRRKPDWAQYHT 787
        |    .Y    | |     ||    |||  |||    | :|   ||||||::::    |
Db 101 YQQIESYYPEVAPHPTQIRSYLREPYYSRLPPPPQP---HPSLDELHRRKEIMAQLEE 156

Qy 788 QKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSC 847
                :| |   |:| :| :  |   :       : :    |::: |||||| ||||
Db 157 RK---VISPPFFA-PSPTLP-PTHPEEFLDEDLKVAG-KYKGNDYSQYSPWSCDTIGSY 210

Qy 848 INAIDSEPKDVIANSNAVLMDLDSGDVKRVHLFETQRTKE--EDPIPFSDGPIISKW 905
        | | |  |||| | |  |:|  :| ::||:  | ::|       |:|| | |  ||
Db 211 IGTKDAKPKDVVAAGSVEMMNVESKGM--RDQRLDLQRRAAETSDDLLPFGDRPTVSRF 268

Qy 906 GAISRSSRTGYHTTDPVQATASQGSAATKPISVSDYVPYVNAVDSRW--SSYG--NEATSS 961
        |||||::   |  ||  | :|: | ||||  ||||  |   | :     | |    | :|
Db 269 GAISRTSKIIYQGRAGPMQAMAPQGAPTKSINISDSPY--GTHGGWGASPYSPHONIPSQ 326

Qy 962 AHYVERDRFIVTDLSGHRK--HSSTGDLLSLSELQQ------------AKSNSLLLQR 1004
         ::||||| |:| | |     ||||||||| | |||             ||||||| |
Db 327 GHFSERERISMSEVASHGKPLPSAEREQLRLELQQLNHQISQQTQLRGPEAVSNRLVLQR 386
```

```
Qy   1005  EANALAMQQ-----------------KWNSLDEGRHLTLNL--LSKEIELRNGELQSDYTEDATDIKPD  1054
Db    387  EANTLAGQSQPPPPPPPPKWPGMISSEQLSLELHQVRREIGKRTELSMB-NQCSLDMK--  443

Qy   1055  RDIELELSALDTDE--PDGQSEPIEEILIDIQLGISSQONDQOLLNGMAVENGHPVQOHQOKEP  1112
Db    444  ----------------SKLNTSKQAENGQOPEPQONKV-------PAEDLTLTFSDVPNGSALTQENISL  488

Qy   1113  PKQKKQSL  1120
Db    489  LSNKTSSL  496
```

RESULT 5
US-09-854-856-36
Sequence 36, Application US/09854856
Patent No. 6541252
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6541252e1 Human Kinases and Polynucleotides
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0178-USA
CURRENT APPLICATION NUMBER: US/09/854,856
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 60/206,015
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 2185
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)..(2185)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-36

Query Match   3.1%; Score 194; DB 2; Length 2185;
Best Local Similarity   18.5%; Pred. No. 1e-05;
Matches 235; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

```
Qy     48  KACPFDQTAINT----------------DIDVLPVNFALLQLVGAQVPDHQSIKLSNLGEN   92
Db    315  KRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLEMATSEYP-------------  361

Qy     93  KHYEVAKKCVEDLALYLKPLSGGKGVASLNQSAL---------------SRPMQRKLVTLVN  139
Db    362  ------YSECQNAAQIYRVTSGVK-PASFDKVAIPEVKEIIEGGIRQNKDERYSIKDLLN  415

Qy    140  CQLVEEGRVRAMRAARSLGERTVTELILQHONPQQLSANLWAAVRARGCQFLGPAMQEE  199
Db    416  HAFFQEETGVRVELAEEDDGEKIAIKLMRIEDIKKLK-------------GKYKDNE  460

Qy    200  ALKLVLLALEDGSALSRKVLVLFVVQRLPRPFPQASKTSIGHVVQLLYRASCFKVTKRDE  259
Db    461  AIEF------------------SFDLERDVPEDVAQEMVESGYVCEGDHKTMAKAIKDR--  501

Qy    260  DSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLAHKSHMQSIID  319
Db    502  -VSLIKRKEQR--QLVREEQEKK--------------KOEESSLKQQVEQSSASQTGIK  544

Qy    320  KLQSPSPSFAKSVQELTIVLQRTGDP-----ANLNRLRPHLELLANIDPNDDAVSPTW  371
Db    545  QLPSASTGIPTASTTSASVSTQVPEEPEADOHQOLQYCQPSISVLS--DGTVDSGQGSS  602

Qy    372  EQLENAMVAVKTVVHGLVLDFIQNYSRKGHET--------------POPQPNSKYKTSMCRDL  419
Db    603  VFTESRVSSQQTVSYG-----SQHEQAHSTGTVPGHIPSTVQAOSQPHGVPPSSVAQG  656
```

```
Qy    420  RQQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISV  479
Db    657  QSQSQ-PSSSLTGVSSSQOPIQHPQ----------------QOQGIQQTTAPPQ----  692

Qy    480  IGSTETTGKIVPSTNGISNAENSVSQLLISRSTDSTLRALETVKKVGKVGANGQNAAGPSA  539
Db    693  ------------------QTVQYSLSQ-TSTSSEAT-----TAQPVSQPQA  719

Qy    540  DSVTENKIGSPPKTPVSNVAATSAGPSN--VGTELNSVPQOKSSPPLTRV--------PVYP  591
Db    720  PQVLP-QVSAGKQLPVSQPVPTIQQBEPQIPVATQPSVVPVHSGAHFLPVGQPLPTPLLP-  777

Qy    592  HSENIQYFQDPPRTQIPFEVPQY--PQTGYYPPPPTVPPAGVAAPCVPRFVRSNNVPESSLP-  648
Db    778  ---------QYPVSQIPISTPHVSTAQTGFSSLPITMAAGITQ--PLLTLASSATTAAIPG  827

Qy    649  ------PASMPYADHYSTFSPRDRMNSSPY----QPPP---POPYGPVPPVPSGMYAPV  694
Db    828  VSTVVPSQLP------TLLQPVTQLPSQVHPQLLQPAVQSMGIPANLGQAAEVPLSSGDVL  882

Qy    695  YDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPR  754
Db    883  YQGFPPPRLPPQYPGDSNIAPSSNVASVCIHBTVLXPPMPTEVLATPGYFPTVVQPYVESN  942

Qy    755  TTYPL--------PREPCGHL----KTSCEEQIRRKPDQWAQYHTQKAPLVSSTLPVATQ  802
Db    943  LLVPMGGVGGQVQVSQPGGSLAQAPTTSSQQAVLES----------TQGVSQVAPAEPVAVA  994

Qy    803  SP--TPPSPL-FSVDF--------RADFSEBVSGTKFEEDHLSHYSPWSCCGTIGSCINAI  851
Db    995  QPQATQPTTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGRTTKRHYRKSVRSRHEK  1054

Qy    852  DSEPKDVIAN-----SNAVLMDLDSGDVKRWHLFETQRRTKEEDPIIPFSDGPIISKWG  906
Db   1055  TSRPKLRILNVSNKGDRVVECQLETHNRKMVTKFDLDGDNPEEIATIMWNNDFIL--  1110

Qy    907  AISRSS-----------------RTGYHTTDPVQA-----TASQ--GSATKP  934
Db   1111  AIRRESFVDQVREIIEKADEMLSEDVSVEPBGDOQLESLQGKDYGFSGSGQKLEGEFKQP  1170

Qy    935  ISVSDYVPYVNAVDSRWSSYGNEATSSAHYVERDRFIVTDLSGHRKHSS---TGDLL-SL  990
Db   1171  IPASSMPQQIGIPTS------SLTQVVHSAGR-RFIVSPVPESRLRESKVFPPSITDTV  1222

Qy    991  ELQOAKSNSLLLQREANALAMQQKWNSLDEGRHITLNLLSKEIELRNGELQSDYTEDATD  1050
Db   1223  AASTAQSPGMNLSHSASSLLSLQQAFS------------------ELRRAQM--TEGPNT  1261

Qy   1051  TKPDRD----------------IELELSALDTDEPDGQSEPIEEILD--IQLGISSQONDQ  1092
Db   1262  APPNFSHTGPTFPVVPPFLSSIAGVPTTAAATAPVPATSSPPNDISTSTSVIQSEVTVPTEE  1321

Qy   1093  LINGMAVENGHPVQOHQKEPPKOKKQOSLGEBDHVILEEQKTILPVTSCFSQOPLPVSISNAS  1152
Db   1322  GIAGVATSTGVVTSGGLPIPP----------------VSESPVLSSVVSSITIPAVVSISTTS  1368

Qy   1153  -CLPITTSVS  1161
Db   1369  PSLQVPTSTS  1378
```

RESULT 6
US-10-010-720-36
Sequence 36, Application US/10010720
Patent No. 6858419
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Hansen, Gwenn
APPLICANT: BeltrandelRio, Hector

```
;  APPLICANT: Van Sligtenhorst, Isaac
;  TITLE OF INVENTION: No. 685841se1 Human Kinases and Polynucleotides
;  TITLE OF INVENTION: Encoding the Same, And Uses Thereof
;  FILE REFERENCE: LEX-0382-USA
;  CURRENT APPLICATION NUMBER: US/10/010,720
;  CURRENT FILING DATE: 2002-05-21
;  PRIOR APPLICATION NUMBER: US 60/206,015
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 09/854,856
;  PRIOR FILING DATE: 2000-05-14
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 36
;  LENGTH: 2185
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: VARIANT
;  LOCATION: (1)..(2185)
;  OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-36

Query Match      3.1%;  Score 194;  DB 2;  Length 2185;
Best Local Similarity   18.5%;  Pred. No. 1e-05;
Matches 235;  Conservative 167;  Mismatches 506;  Indels 362;  Gaps 49;

Qy   48  KACPFDQTAINT-------------------------DIDVLPVNFALLQLVSAQVPDHQSIKLSNLGEN  92
                                                :   ::
Db  315  KRASFAKSVIGTPEFMAPEMYEEKYDESGVDVAFGCMLEMATSEYP-----------------------  361

Qy   93  KHYEVAKKCVEDLALYLKPLSGGKGVASLNQSAL-------------------------SRPMQRKLVTLVN  139
                                                                    ::: :::
Db  362  -----------YSECQNAAQIYRRVTVTSGVK-PASFDKVAIPEVKEIIEGCIRQNKDERYSIKDLLN  415

Qy  140  CQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANLWAAVARARGCQFLGPAMQEE  199
                                    :::  ::
Db  416  HAFFQEETGVRVELAEEDDGEKIAIKLWLRIEDIKKLK-----------GKYKDNE  460

Qy  200  ALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQLLYRASCPKVTKRDE  259
                                               :  ::
Db  461  AIEF-----------------SFDLERDVPEDVAQEMVESGYVCEGDHKTMAKAIKDR--  501

Qy  260  DSSIMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLAHKSHMQSIID  319
                                              :::  :
Db  502  -VSLIKRKEQR--QLVREEQEKK-----------KQEESSLKQQVEQSSASQTGIK  544

Qy  320  KLQSPRSFAFKSVQELTIVLQRTGDP-----------ANLNRLRPHLELLANIDPNPDAVSPTW  371
                                                   :::
Db  545  QLPSASTGIPIASTTSASVSTQVEPEPEADQHQLQYQQPSISVLS--DGTVDSGQGSS  602

Qy  372  EQLENANAVAKTVVHGLVDFIQNYSRKGHET----------------PQPQENSKYKTSMCRDL  419
                                                               ::::
Db  603  VFTESRVSSQQTVSYG-----------SQHEQAHSTGTVPHIPSTVQAQSQPHGVPPSSVAQG  656

Qy  420  RQQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTPPLLNKVGVANNTVTTTAGNVISV  479
                                    ::: :::
Db  657  QSQGQ-PSSSLTGVSSSQPIQHPQ-----------QQGIQQTAPPQ-----  692

Qy  480  IGSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVKVGANGQNAAGPSA  539
                                    :::  :
Db  693  --------------QTVQYSLSQ-TSTSSEAT-----------TAQPVSQPQA  719

Qy  540  DSVTENKIGSPPKTPVSNVAATSAGPSN--VGTELNSVPQKSSPFLTRV-----PVTPP  591
                                    :::
Db  720  PQVLP-QVSAGKQLPVSQPVPPTIQGEPQIPVATQPSVVPVHSGAHFPLPVGQPLPTPLLP-  777

Qy  592  HSENIQYFQDPRTQIPEVPQY-----PQTGYYPPPPTVPAGVAPCVPRFVRSNNVPESSLP-  648
                                    :::
Db  778  ----------QYPVSQIPISTPHVSTAQTQFSSLDITMAAGITQ--PLLTLASSATTAAIPG  827

Qy  649  ----PASMPYADHYSTPSPRDRMNSSPY-----QPPP-----PQPYGPVPPPVPSGMYAPV  694
                                    :::
Db  828  VSTVVPSQLP----TLLQPVTQLPSQVHPQLLQPAVQSMGIPANLGQAAEVPLSSGDVL  882
```

```
Query Match      3.1%;  Score 194;  DB 2;  Length 2245;
Best Local Similarity   18.5%;  Pred. No. 1.1e-05;
Matches 235;  Conservative 167;  Mismatches 506;  Indels 362;  Gaps 49;

Qy   695  YDSRRIWRPPMYQRDDIIRSNSLPPMDVMDSSVYQTSLRERYNSLDGYYSVACQPPSEPR  754
              ||||   ||||
Db   883  YQGFPPRLPPQYPGDSNIAPSSNVASVCIHSTVLXPPMPTEVLATPGYFPTVVQPYVESN  942

Qy   755  TTVPL------PREPCGHL----KTSCEEQIRRKPDQWAQYHTQKAPLVSSTLPVATQ  802
              ||||:
Db   943  LLIVPMGGVGGQVQVSQPGGSLAQAPTTSSQQAVLES------TQGVSQVAPAPPVAVA  994

Qy   803  SP--TPPSPL-FSVDF------RADFSEBSVSGTKFEEDHLSHYSPSWSCCGTIGSCINAI  851
              ||||
Db   995  QPQATQPPTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGRTTKRHYRKSVSRSRHEK  1054

Qy   852  DSEPKDVIAN----SNAVLMDLDSGGDVKRRVHLFETQRRTKEEDPIIPFSDGPIISKWG  906
              ||||:
Db  1055  TSRPKLRILNVSNKGDRVVECQLETHNRKMVTFKPDLDGDNPEEIATIMVNNDFIL----  1110

Qy   907  AISRSS------RTGYHTTDPVQA------TASQ----GSATKP  934
              ||||
Db  1111  AIERESFVDQVREIIEKADEMLSEDVSVPFPEGDQGLESLQGKDDYGFSGSGSQKLEGEFKQP  1170

Qy   935  ISVSDYVPYVVNAVDSRWSSYGNEATSSAHYVERDRFIVTDLSGHRKHSS---TGDLL-SL  990
              ||||:
Db  1171  IPASSMPQQIGIPTS-----SLTQVVHSAGR-RFIVSPVPESRLRESKVFPSEITDTV  1222

Qy   991  ELQQAKSNSILLQRBEANALAMQQKWNSLDEGRHITLNLLSKEIELRNGELQSDVTEDATD  1050
              ||||:
Db  1223  AASTAQSPGMNLSHSASSLSLQQAFS------ELRRAQM---TEGPNT  1261

Qy  1051  TKPDRD------IELELSALDTDEPDGQSEPIEEILD--IQLGISSQNDQ  1092
              ||:
Db  1262  APPNFSHTGPTFPVVPPFLSSIAGVPTTAAATAPVPATSSPPNDISTSTSVIQSEVTVPTEE  1321

Qy  1093  LINGMAVENGHPVQQHQKEPPKQKKQSLGBDHVILEEQKTILPVTSCFSQPLPVSISNAS  1152
              ||||
Db  1322  GIAGVATSTGVVTSGGLPIPP------VSESPVLSSVVSSITIPAVVSISTTS  1368

Qy  1153  -CLPITTSVS  1161
              |:|||
Db  1369  PSLQVPTSTS  1378
```

```
RESULT 8
US-10-010-720-4
Sequence 4, Application US/10010720
Patent No. 6858419
GENERAL INFORMATION:
  APPLICANT: Walke, D. Wade
  APPLICANT: Hilbun, Erin
  APPLICANT: Donoho, Gregory
  APPLICANT: Turner, C. Alexander Jr.
  APPLICANT: Hansen, Gwenn
  APPLICANT: BeltrandelRio, Hector
  APPLICANT: Van Sligtenhorst, Isaac
  TITLE OF INVENTION: No. 6858419el Human Kinases and Polynucleotides
  TITLE OF INVENTION: Encoding the Same, And Uses Thereof
  FILE REFERENCE: LEX-0382-USA
  CURRENT APPLICATION NUMBER: US/10/010,720
  CURRENT FILING DATE: 2002-05-21
  PRIOR APPLICATION NUMBER: US 60/206,015
  PRIOR FILING DATE: 2000-05-19
  PRIOR APPLICATION NUMBER: US 09/854,856
  PRIOR FILING DATE: 2000-05-14
  NUMBER OF SEQ ID NOS: 64
  SOFTWARE: FastSEQ for Windows Version 4.0
US-10-010-720-4
SEQ ID NO 4
  LENGTH: 2245
  TYPE: PRT
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: VARIANT
  LOCATION: (1)...(2245)
  OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-4

Query Match             3.1%;  Score 194;  DB 2;  Length 2245;
Best Local Similarity  18.5%;  Pred. No. 1.1e-05;
Matches  235;  Conservative 167;  Mismatches 506;  Indels 362;  Gaps 49;
```

```
Qy   48 KACPFDQTAINT----...----DIDVLPVNFALLQLVGAQVPDHQSIKLSNLGEN    92
Db  375 KRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLEMATSEYP----------   421
Qy   93 KHYEVAKKCVEDLALYLKPLSGGKGVASLNQSAL----...----SRPMQRKLVTLVN  139
Db  422 -YSECQNAAQIYRRVTSGVK-PASFDKVAIPEVKEIIEGCIRQNKDERYSIKDLLN    475
Qy  140 COLVEEGRVRAMRAARSLGERTVTELILLQHQNPQQLSANLWAAVRARGCQFLGPAMQEE 199
Db  476 HAFFQEETGVRVELAEEDDGEKIAIKLWLRIEDIKKLK----...----GKYKDNE    520
Qy  200 ALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQLLYRASCFKVTKRDE 259
Db  521 AIEF----...----SFDLERDVPEDVAQEMVESGYVCEGDHKTMAKAIKDR--      561
Qy  260 DSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLAHKSHMQSIID 319
Db  562 -VSLIKRKEQR--QLVREEQEKK----...----KQEESLKQQVEQSSASQTGIK     604
Qy  320 KLQSPSFSAKSVQELTIVLQRGDP----...----ANLNRLRFHLELLANIDPNPDAVSPTW 371
Db  605 QLPSASTGIPTASTTSASVSTQVEPEEPEADQHQQLQYQQPSISVLS--DGTVDSGQSS 662
Qy  372 EQLENAMVAKVTVVHGLVDFIQNYSRKGHET----...----PQPQPNSKYKTSMCRDL 419
Db  663 VFTESRVSSQQTVSYG----...----SQHEQAHSTGTVPGHIPSTVQAQSQPHGVVPPSSVAQG 716
Qy  420 ROQGGCPRGTNCTFAHSQEELEKVRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISV 479
Db  717 QSQGQ-PSSSLTGVSSSQPIQHPQ----...----QQOGIQQTAPPQ              752
Qy  480 IGSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGVGANGQNAAGPSA 539
Db  753 -------QTVQYSLSQ-TSTSSEAT----...----TAQPVSQPQA              779
Qy  540 DSVTENKIGSPPKTPVSNVAATSAGPSN--VGTELNSVPQKSSPFLTRV----...----PVYPP 591
Db  780 PQVLP-QVSAGKQLPVSQPVPTIQGEPQIPVATQPSVVPHSGAHFLPVGQPLPTLLP-  837
Qy  592 HSENIQYFQDPRTQIPFEVPQY--PQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLP  648
Db  838 -------QYPVSQIPISTPHVSTAQTGFSSLPITMAAGITQ----...----PLLTLASSATTAAIPG 887
Qy  649 -----PASMPYADHYSTFSPRDRMNSSPY---QPPP----...----PQPYGVPVPPVSGMYAPV 694
Db  888 -----TLLQPVTQLPSQVHPQLIQPAVQSMGIPANLGQAAEVPLSSGDVL         942
Qy  695 YDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQTSLRERYNSLDGYYSVACQPPSPER 754
Db  943 YQGFPPRLPPQYPGDSNIAPSSNVASVCIHSTVLXPMPTEVLATPGYTFPTVVQPYVESN 1002
Qy  755 TTVPL----...----PREPCGHL----...----KTSCEEQIRRKPDQWAQVHTQKAPLVSSTLPVATQ 802
Db 1003 LLIVPMGGVGQGVQVSQPGGSLAQAPTTSSQQAVLES----...----TQGVSQVAPAEPAVA 1054
Qy  803 SP--TPPSPL-TSVDF----...----RADFSESVSGGTKFEEDHLSHYSPWSCGTIGSCINAI 851
Db 1055 QPQATQPTTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGRTKRHYRKSVRSRSHEK  1114
Qy  852 DSEPKDVIAN----...----SNAVIMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGPIISKWG 906
Db 1115 TSRPKLRILNVSNKGDRVUCQLETHNRKMVTFKPDLDGDNPEEIATIMVNNDFIL--   1170
Qy  907 AISRSS----...----RTGYHTTDPVQA----...----TASQ---GSATKP       934
Db 1171 AIERESFVDQVREIIEKADEMLSEDVSVEPEGDQGLESLQGKDDYGFSGSQKLEGEFKQP 1230
Qy  935 ISVSDYPYVNAVDSRWSSYGNEATSSAHYVERDRFIVTDLSGHRKHSS---TGDLL-SL  990
Db 1231 IPASSMPQQIGIPTS----...----SLTQVVHSAGR-RFIVSPVPESRLRESKVFPSEITDTV 1282
Qy  991 ELQQAKSNSLLLQREANALAMQQKWNSLDEGRHLTLNLLSKEIELRNGELQSDYTEDATD 1050
Db 1283 AASTAQSPGMNLSHSASSLSLLQQAFS----...----ELRAQM----TEGPNT      1321
Qy 1051 TKPDRD----...----IELELSALDTDEPPDGQSEPIEBILD--IQLGISSQNDQ    1092
Db 1322 APPNFSHTGPTPVVPPFLSSIAGVPTTAAATAPVPAATSSPPNDISTSVIQSEVTVPTEE 1381
Qy 1093 LLNGMAVENGHPVQOHOKEPFPPKQKKQSLGEDHVILEEQKTILPVTSCFSQPLPVSISNAS 1152
Db 1382 GIAGVATSTGVVTSGGLPIPP----...----VSESPVLSSVVSSIIPAVVSISTTS   1428
Qy 1153 -CLPITTSVS 1161
Db 1429 PSLQVPTSTS 1438
```

RESULT 9
US-09-854-856-34
; Sequence 34, Application US/09854856

```
Qy    320  KLQSPESFAKSVQELTIVLQRTGDP----------ANLNRLRPHLELLANIDPNPDAVSPTW    371
           |||||||||||||||||||||||||                   |||||||||||||||||||
Db    605  QLPSASTGIPTASTTSASVSTQVEPEPEADQHQQLQYQQPSISVLS--DGTVDSGQGSS     662

Qy    372  EQLENAMVAVKTVVHGLVDFIQNYSRKGHET----------PQPQPNSKYKTSMCRDL     419
           :  ::|||||||||||                                  |::|| ||
Db    663  VFTESRVSSQQTVSYG----------SQHEQAHSTGTVPGHIPSTVQAQSQPHGVYPPSSVAQG     716

Qy    420  RQQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISV     479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    717  QSQGQ-PSSSLTGVSSSQPIQHPQ----------QQQGIQQTAPPQ-------------     752

Qy    480  IGSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSA     539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    753  -------------------------------------------QTVQYSLSQ-TSTSSEAT     779

Qy    540  DSVTENKIGSPPKTPVSNVAATSAGPSN--VGTELNSVPQKSSPFLTRV------PVYPP     591
           |||||||||||||||||||||||||||      ::| ||::|| ||       ||||
Db    780  PQVLP-QVSAGKQLPVSQPVPTIQGEPQIPVATQPSVPVHSGAHFLPVGQPLPTPLLP-     837

Qy    592  HSENIQYFQDPRTQIPFEVPQY---PQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLP-     648
           ||||||||||||||||||||||      :: ||||||||||||||||||||||||||||
Db    838  -------QYPVSQIPISTPHVSTAQTGFSSLPITMAAGITQ--PLLTLASSATTAAIPG     887

Qy    649  -----PASMPYADHYSTFSPRDRMNSSPY-----QPPP----POPYGPVPVPSGMYAPV     694
           ||                                        ||::::::|| ||
Db    888  VSTVVPFSQLP--------------TLLQPVTQLPSQVHPQLLQPAVQSMGIPANLGQAAEVPLSSGDVL     942

Qy    695  YDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPR     754
           ::| |           : :| :|              |:||| ::|         |||
Db    943  YQGFPPRLPQQYPGDSNIAPSSNVASVCIHSTVLIXPPMPTEVLATPGYFPTVVQPYVESN     1002

Qy    755  TTVPL------------PREPCGHL------KTSCEEQIRRKPDWAQYHTQKAPLVSSTLPVATQ     802
           ::|                                |  :|       |: :||||:
Db   1003  LLVPMGGVGGQVQVSQPCGSLAQAPTTSSQQAVLES----------TQSVSQVPAPEPVAVA     1054

Qy    803  SP--TPPSPL-FSVDF----RADFSESVSGTKFEEDHLSHYSPWSCGTIGSCINAI     851
           ||        |||                                      |:||| :
Db   1055  QPQATQPTTLASSVDSAHSDVASGMSDGNENVPSSGRHEGRTTKRHYRKSVRSRSRHEK     1114

Qy    852  DSEPKDVIAN----------SNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGPIISKWG     906
           ||||      :                  | |||:  |:|||::::||  |||  | |:||||
Db   1115  TSRPKLRILNVSNKGDRVVECQLETHNRKMVTFKFDLDGDNPEEIATIMVNNDFIL---     1170

Qy    907  AISRSS----------------RTGYHTTDPVQA-----TASQ---GSATKP     934
           ||:                      | ||  :||||              ||||
Db   1171  AIERESFVDQVREIIEKADEMLSEDVSVEPEGDQGLESLQGRDDYGFSGSGSQKLEGERKQP     1230

Qy    935  ISVSDVPYVNAVDSRWSSYGNEATSSAHYVERDRFIVTDLSGHRKHSS---TGDLL-SL     990
           ||||||||||||||||||||||||||||||||||||||||||||||||    |||| ||
Db   1231  IPASSMPQQIGIPTS----------SLIQVVHSAGR-RFIVSPVPESRLRESKVFPSEITDTV     1282

Qy    991  ELQQAKSNSLILQREANALAMQQKWNSLDEGRHLTLNLLSKEIELRNGELQSDYTEDATD     1050
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1283  AASTAQSPGMNLSHSASSLSLQQAFS----------ELRRAQM---TEGPNT     1321

Qy   1051  TKPDRD----------IELELSALDTDEPDGQSEPIEEILD--IQLGISSQNDQ     1092
           |||                                         ||::| :||||
Db   1322  APPNFSHTGPTPFPVVPPFLSSIAGVPPTLAAATAPVPATSSPPNDISTSVIQSEVTVPTEE     1381

Qy   1093  LLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCFSQPLPVSISNAS     1152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1382  GIAGVATSTGVVTSGGLPIPP----------VSESPVLSSVVSSITIPAVVSISTTS     1428

Qy   1153  -CLPITTSVS     1161
           :|      ||
Db   1429  PSLQVPTSTS     1438
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Query Match   3.1%; Score 194; DB 2; Length 2322;
Best Local Similarity   18.5%; Pred. No. 1.1e-05;
Matches 235; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

```
Qy     48  KACPFDQTAINI---------------------DIDVLPVNFALLQLVGAQVPDHQSIKLSNLGEN     92
           ||||                                :  :||  :|:| |||  :|| :||
Db    315  KRASFAKSVIGTPEFMAPEMYEEKVDESVDVYAFGMCMLEMATSEYP---------------     361

Qy     93  KHYEVAKKCVEDLALYLKPLSGGKGVASLNQSAL--------------SRPMQRKLVTLVN     139
           ||||                                                |  : |||
Db    362  -----YSECQNAQIYRVTSGVK--PASPDKVAIPEVKEIIEGCIRQNKDERYSIKDLLN     415

Qy    140  CQLVEEEGRVRAMRAARSLGERTVTELIIQHQNPQQLSANLWAAVRARGCQFLGPAMQEE     199
           ||||                                                        ||:||
Db    416  HAFFQEETGVRVELAEEDDGEKIAIKLWLRIEDIKKLK-----------GKYKDNE     460

Qy    200  ALKLVILLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQLLYRASCFKVTKRDE     259
           |||                                           |:|| :|||||||||
Db    461  AIEP----------------SFDLERDVPEDVAQEMVESGYVCEGDHKTMAKAIKDR-     501

Qy    260  DSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSLLYGDLAHKSHMQSIID     319
           |||                                                          |||
Db    502  -VSLIKRKREQR--QLVRBEQEKK-----------------KQEESSLKQQVEQSSASQTGIK     544

Qy    320  KLQSPESFAKSVQELTIVLQRTGDP----------ANLNRLRPHLELLANIDPNPDAVSPTW     371
           ||||||||||||||||||||||||||                   ||||||||||||||||||||
Db    545  QLPSASTGIPTASTTSASVSTQVEPEPEADQHQQLQYQQPSISVLS--DGTVDSGQGSS     602

Qy    372  EQLENAMVAVKTVVHGLVDFIQNYSRKGHET----------PQPQPNSKYKTSMCRDL     419
           :  ::||||||||||                                  |::|| ||
Db    603  VFTESRVSSQQTVSYG----------SQHEQAHSTGTVPGHIPSTVQAQSQPHGVYPPSSVAQG     656

Qy    420  RQQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISV     479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    657  QSQGQ-PSSSLTGVSSSQPIQHPQ----------QQQGIQQTAPPQ-------------     692

Qy    480  IGSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSA     539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    693  -------------------------------------------QTVQYSLSQ-TSTSSEAT     719

Qy    540  DSVTENKIGSPPKTPVSNVAATSAGPSN--VGTELNSVPQKSSPFLTRV------PVYPP     591
           |||||||||||||||||||||||||||      ::| ||::|| ||       ||||
Db    720  PQVLP-QVSAGKQLPVSQPVPTIQGEPQIPVATQPSVPVHSGAHFLPVGQPLPTPLLP-     777

Qy    592  HSENIQYFQDPRTQIPFEVPQY---PQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLP-     648
           ||||||||||||||||||||||      :: ||||||||||||||||||||||||||||
Db    778  -------QYPVSQIPISTPHVSTAQTGFSSLPITMAAGITQ--PLLTLASSATTAAIPG     827
```

```
RESULT 10
US-10-010-720-34
Sequence 34, Application US/10010720
Patent No. 6858419
GENERAL INFORMATION:
 APPLICANT: Walke, D. Wade
 APPLICANT: Hilbun, Erin
 APPLICANT: Donoho, Gregory
 APPLICANT: Turner, C. Alexander Jr.
 APPLICANT: Hansen, Gwenn
 APPLICANT: BeltrandelRio, Hector
 APPLICANT: Van Sligtenhorst, Isaac
 TITLE OF INVENTION: No. 6858419el Human Kinases and Polynucleotides
 TITLE OF INVENTION: Encoding the Same, And Uses Thereof
 FILE REFERENCE: LEX-0382-USA
 CURRENT APPLICATION NUMBER: US/10/010,720
 CURRENT FILING DATE: 2002-05-21
 PRIOR APPLICATION NUMBER: US 60/206,015
 PRIOR FILING DATE: 2000-05-19
 PRIOR APPLICATION NUMBER: US 09/854,856
 PRIOR FILING DATE: 2000-05-14
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
 LENGTH: 2322
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
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```
 NAME/KEY: VARIANT
 LOCATION: (1)...(2322)
 OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-34
Query Match   3.1%;  Score 194;  DB 2;  Length 2322;
Best Local Similarity 18.5%;  Pred. No. 1.1e-05;
Matches 235;  Conservative 167;  Mismatches 506;  Indels 362;  Gaps 49;
```

```
Qy   649  -----PASMPYADHYSTFSPRDRMNSSPY----QPPP----PQPYGPVPVPSGMYAPV   694
              :::::                                  :
Db   828  VSTVVPSQLP-----TLLQPVTQLPSQVHPQLLQPAVQSMGIPANLGQAAEVPLSSGGDVL   882

Qy   695  YDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPR   754
          ::::                                                    :
Db   883  YQGFPPRLPPQYPGDSNIAPSSNVASVCIHSTVLXPPMPTEVLATPGYFPTVVQPYVESN   942

Qy   755  TTVPL-------PREPCGHL-----KTSCEEQIRRKPDQWAQYHTQKAPLVSSTLPVATQ   802
                                    :
Db   943  LLVPMGGVGGQVQVSQPGGSLAQAPTTSSQQAVLES------TQSVSQVAPAEPVAVA   994

Qy   803  SP--TPPSPL-FSVDF------RADFSESVSGTKFEEDHLSHYSPWSCGTTIGSCINAI   851
          ::   :::::  :::::       :::::
Db   995  QPQATQPTTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGRTKRHYRKSVRSRSRHEK   1054

Qy   852  DSEPKDVIAN-----SNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGPIISKWG   906
                                 :::  :
Db   1055 TSRPKLRILNVSNKGDRVVECQLETHNRKMVTFKFDLDGDNPEEIATIMVNNDFIL----   1110

Qy   907  AISRSS-------RTGYHTTDPVQA------TASQ---GSATKP   934
Db   1111 AIERESFVDQVREIIEKADEMLSEDVSVEPEGDQGLLESLQGKDDYGFSGSQKLEEGEKQP   1170

Qy   935  ISVSDVYPYVNAVDSRWSSYGNEATSSAHYVERDRFIVTDLSGHRKHSS---TGDLL-SL   990
          :::::                              ::::                ::
Db   1171 IPASSMPQQIGIPTS------SLTQVVHSAGR-RFIVSPVPESRLRESKVFPSEITDTV   1222

Qy   991  ELQQAKSNSLLLQREANALAMQQKWNSLDEGRHLTLNLLSKEIELRNGELQQSDYTEDATD   1050
Db   1223 AASTAQSPGMNLSHSASSLSLQQAFS----------ELRRAQM---TEGPNT   1261

Qy   1051 TKPDRD-------IELELSALDTDEPDGQGSEPIEEILD--IQLGISSQNDQ   1092
              :                                       ::
Db   1262 APPNFSHTGPTPEVVPPLSSIAGVPTTAAAATAPVPATSSPPNDISTSVIQSEVTVPTEE   1321

Qy   1093 LLNGMAVENGHFVQQQHOKEPPKQKKQSLGEDHVILEEQKTILPVTSCFSQPLPVSISNAS   1152
Db   1322 GIAGVATSTGVVTSGGLPIPP------VSESPVLSSVVSSITIPAVVSISTTS   1368

Qy   1153 -CLPITTSVS   1161
              ::::
Db   1369 PSLQVPTSTS   1378
```

```
Qy   48   KACPFDQTAINT-------------------DIDVLPVNFALLQLVGAQVPDHQSIKLSNLGEN   92
          :::                            :::
Db   315  KRASFAKSVIGTPEFMAPEMYEEKYDESVDVYARGMCMLBMATSEYP------   361

Qy   93   KHYEVAKKCVEDLALYLKPLSGGKGVASLNQSAL----------SRPMQRKLVTLVN   139
          ::                                          ::: :
Db   362  -----YSECQNAAQIYRRVTSGVK-PASFDKVALPEVKEIIEGGCIRQNKDERYSIKDLLN   415

Qy   140  CQLVEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANLWAAVRARGCQFLGPAMQEE   199
Db   416  HAFFQEETCVRVELAEEDDGEKIAIKLWLRIEDIKKLK------GKYKDNE   460

Qy   200  ALKIVLLALEDGSALSRKVLVLFVVQRLEPRFFQQASKTSIGHVVQLLYRASCFKVTKRDE   259
Db   461  AIEF---------------SFDLERDVPEDVAQEMVESGYVCEGDHKTMAKAIKDR--   501

Qy   260  DSSIMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLAHKSHMQSIID   319
          :::                             ::::
Db   502  -VSLIKRREQR--QLVREEQEKK-----------------KQEESLKQQVEQSSASQTGIK   544

Qy   320  KLQSPESFAKSVQELTIVLQRTGDP--------ANLNRLRPHLELLANIDPNDPAVSPTW   371
          :::                             :
Db   545  QLPSSASTGIPTPASTTSASVSTQVEPEEPEADQHQQLQYQOPSISVLS--DGTVDSGQGSS   602

Qy   372  EQLENAMVAVKTVVHGLVDFIQNYSRKGHET----------PQPQPNSKYKTSMCRDL   419
Db   603  VFTESRVSSQQTVSYG------SQHEQAHSTGTVPGHIPSTVQAQSQPHGVYPSSVAQG   656

Qy   420  RQQQGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISV   479
          ::                                                   ::
Db   657  QSQSQ-PSSSSLTGVSSSQPIQHPQ--------QQQQIQQTAPPQ   692

Qy   480  IGSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSA   539
Db   693  ------QTVQYSLSQ-TSTSSEAT----------TAQPVSQPQA   719

Qy   540  DSVTENKIGSPPKTFPVSNVAATSAGPSN--VGTELNSVPQKSSPFLTRV----PVYPP   591
          :::                                                   ::::
Db   720  PQVLP-QVSAGKQLPVSQVPVPTIQGEPQIPVATQPSVVPVHSGAHFLPVGQPLPTPLLP-   777

Qy   592  HSENIQYFQDPRTIQLPFEVPQY--PQTGYYPPPPYPAGVAPCVPRFVRSNNVPESSLP-   648
          :::::                    :::
Db   778  -------QYPVSQIPISTPHVSTPAQTGFSSLPITMAAGITQ--PLLTLASSATTAAIPG   827

Qy   649  -----PASMPYADHYSTFSPRDRMNSSPY----QPPP----PQPYGPVPVPSGMYAPV   694
              :::::                                  :
Db   828  VSTVVPSQLP-----TLLQPVTQLPSQVHPQLLQPAVQSMGIPANLGQAAEVPLSSGGDVL   882

Qy   695  YDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPR   754
          ::::
Db   883  YQGFPPRLPPQYPGDSNIAPSSNVASVCIHSTVLXPPMPTEVLATPGYFPTVVQPYVESN   942

Qy   755  TTVPL-------PREPCGHL-----KTSCEEQIRRKPDQWAQYHTQKAPLVSSTLPVATQ   802
             :
Db   943  LLVPMGGVGGQVQVSQPGGSLAQAPTTSSQQAVLES------TQSVSQVAPAEPVAVA   994

Qy   803  SP--TPPSPL-FSVDF------RADFSESVSGTKFEEDHLSHYSPWSCGTTIGSCINAI   851
          ::   :::::  :::::       :::::
Db   995  QPQATQPTTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGRTTKRHYRKSVRSRSRHEK   1054

Qy   852  DSEPKDVIAN-----SNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGPIISKWG   906
Db   1055 TSRPKLRILNVSNKGDRVVECQLETHNRKMVTFKFDLDGDNPEEIATIMVNNDFIL----   1110
```

```
Qy    907 AISRSS-----------------------RTGYHTTDPVQA------TASQ---GSATKP 934
          |:|:|                        ||:|:|
Db   1111 AIERESFVDQVREIIEKADEMLSEDVSVEPEDGDQGLESLQGSQKLEGERKQP 1170

Qy    935 ISVSDYPYVNAVDSRWSSYGNEATSSAHYVERDRFIVTDLSGHRKHSS---TGDLL-SL 990
          ||:.:                                 ||||::.       ||||  ||
Db   1171 IPASSMPQQIGIPTS----------SLTQVVHSAGR-RFIVSPVPESRLRESKVFPSEITDTV 1222

Qy    991 ELQQAKSNSLLLQREANALAMOQKWNSLDEGRHLTLNLLSKIELRNGELQSDYTEDATD 1050
          ||||||||||||                              ||||||
Db   1223 AASTAQSPGMNLSHSASSLSLQQAFS------------------ELRRAQM----TEGPNT 1261

Qy   1051 TKPDRD------------------------IELELSALDTDEPDGQSEPIEEILD--IQLGISSQNDQ 1092
          ||||||                        :|
Db   1262 APPNFSHTGTPFVVPPFLSSIAGVPTTAAATAPVPATSSPPNDISTSVIQSEVTVPTEE 1321

Qy   1093 LLNGMAVENGHPVQOHQKEPPRKOKKQSLGEBDHVILEEQKTILPVTSCFSQPLPVSISNAS 1152
          |||
Db   1322 GIAGVATSTGVVTSGGLPIPP-----------------VSESPVLSSVVSSITIPAVVSISTTS 1378

Qy   1153 -CLPITTSVS 1161
           ::|
Db   1369 PSLQVPTSTS 1378
```

RESULT 11
US-09-854-856-2
Sequence 2, Application US/09854856
Patent No. 6541252
GENERAL INFORMATION:
  APPLICANT: Walke, D. Wade
  APPLICANT: Hilbun, Erin
  APPLICANT: Donoho, Gregory
  APPLICANT: Turner, C. Alexander Jr.
  TITLE OF INVENTION: No. 65412S2el Human Kinases and Polynucleotides
  TITLE OF INVENTION: Encoding the Same
  FILE REFERENCE: LEX-0178-USA
  CURRENT APPLICATION NUMBER: US/09/854,856
  CURRENT FILING DATE: 2001-05-14
  PRIOR APPLICATION NUMBER: US 60/206,015
  PRIOR FILING DATE: 2000-05-19
  NUMBER OF SEQ ID NOS: 64
  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
  LENGTH: 2382
  TYPE: PRT
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: VARIANT
  LOCATION: (1)...(2382)
  OTHER INFORMATION: Xaa = Any Amino Acid

Query Match   3.1%; DB 2; Length 2382;
Best Local Similarity 18.5%; Pred. No. 1.2e-05;
Matches 235; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

Score 194;

```
Qy     48 KACPFDQTAINT---------------DIDVLPVNFALLQLVGAQVPDHQSIKLSNLGEN 92
          ||:|
Db    375 KRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLEMATSEYP-------------421

Qy     93 KHYEVAKKCVEDLALYLKPLSGGKGVASLNQSAL----------SRPMQRKLVTLVN 139
          :||                                          :|:|
Db    422 -----YSECQNAAQIYRRVTSGVK-PASFDKVAIPEVKEIIEGCIRQNKDERYSIKDLLN 475

Qy    140 COLVEEGRVRAMRAARSLGERTVTELILIQHONPQQLSANLWAAVRARGCQFLGPAMQEE 199
          |:|                                     |:|
Db    476 HAFFQEETGVRVELAEBDDGEKIAIKLWLRIEDIKKLK----------GKYKDNE 520

Qy    200 ALKVLLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQLLYRASCFKVTKRDE 259
          |:|                             :|:
Db    521 AIEF----------------SFDLERDVPEDVAQOEMVESGYVCEGDHKTMAKAIKDR--561

Qy    260 DSSLMQLKEEPRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLAHKSHMQSIID 319
          ::|                                   :|:
Db    562 -VSLIKRKREQR--QLVREEQEKK-------------KQEEESSLKQQVEQSSASQQTGIK 604

Qy    320 KLQSPESFAKSVQELTIVLQRTGDP--------ANINLRLPHLELLANIDPNPDAVSPTW 371
          ||:||||:|||||                    |||||||:||||||
Db    605 QLFSASTGIPLTASTTSASVSTQVEPEPEADHOQLQYQOPSISVLS--DGTVDSGQGSS 662

Qy    372 EQLENAMVAVKTVVHGLVDFIQNYSRKGHET-------------PQPQPNSKYKTSMCRDL 419
          |:|                                        ||:|
Db    663 VFTESRVSSQOOTVSYG--------SQHEQAHSTGTVPGHIPSTVQAQSQPHGVYPFSSVAQG 716

Qy    420 IGSTETTGKIVPSTNGISNAENSVSQLLSRSTDSTSTLRALETVKKVGKVGANGQNAAGPSA 479
          ||:||||||                  :|:
Db    717 ----QSPQQ-PSSSLTGVSSSQPIQHPQ---------QTVQYSLSQ-TSTSSEAT 752

Qy    480 DSVTENKIGSPPKPTPVSNVAATSAGPSN--VGTELNSVPQKSSPFLTRV------PVYPP 539
          ::|                             :|:
Db    753 PQVLP-QVSAGKQLPVSQPVPTIQGEPQIPVATQPSVVPVHSGAHFLPVGQPLPTPLLP- 837

Qy    592 HSENIQYFQDPRTIQIPFEVPQY--PQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLP- 648
          ::|
Db    838 ------QYPVSQIPISTPHVSTAQTGFSSLPITMAAGITQ--PLITLASSATTAAIPG 887

Qy    649 -----PASMPYADHYSTFSPRDRMNSSPY-----QPPP----PQPYGPVPPVPSGMYAPV 694
          ::|
Db    888 VSTVVPSQLP--------TLLQPVTQLPSQVHPQLLQPAVQSMGIPANILGQAAEVPLSSGDVL 942

Qy    695 YDSRRIWRPPMYQRDDIIRSNSLPPMDVWHSSVYQTSLRERYNSLDGYYSVSVACQPPSEPR 754
          |||
Db    943 YQGFPPRLPPQYPGDSNIAPSSNVASVCIHSTVLXPMPTEVLATPGYPFTIVVQOPYVESN 1002

Qy    755 TTVPL----------PREPCGHLI----KISCEEQIRRKPDQWAQYHTQKAPLVSSTLPVATQ 802
          ::|:
Db   1003 LLVPMGGVGGQVQVSQPGGSLAQAPTTSSQQAVLES-----------TQGVSQVAPAEPVAVA 1054

Qy    803 SP--TPPSPL-FSVDP----------RADFSESVSGTKFEEDHLSHYSPWSCGTIGSCINAI 851
          ::|
Db   1055 QFPQATQPTTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGRTTKRHYRKSVRSRSRHEK 1114

Qy    852 DSBPKDVIAN------SNAVLMDLDSGDVKRRVLHFETQRRTKEEDPIPFSDGPIISKWG 906
          ::|
Db   1115 TSRPKLRLINVSNKGDRVVEBCQLETHNRKMVTFKFDLDGDNPEEIATIMVNNDFIL-- 1170

Qy    907 AISRSS-----------------------RTGYHTTDPVQA------TASQ---GSATKP 934
          |:|:|                        ||:|:|
Db   1171 AIERESFVDQVREIIEKADEMLSEDVSVEPEDGDQGLESLQGSQKLEGERKQP 1230

Qy    935 ISVSDYPYVNAVDSRWSSYGNEATSSAHYVERDRFIVTDLSGHRKHSS---TGDLL-SL 990
          ||:.:                                 ||||::.       ||||  ||
Db   1231 IPASSMPQQIGIPTS----------SLTQVVHSAGR-RFIVSPVPESRLRESKVFPSEITDTV 1282

Qy    991 ELQQAKSNSLLLQREANALAMOQKWNSLDEGRHLTLNLLSKIELRNGELQSDYTEDATD 1050
          ||||||||||||                              ||||||
Db   1283 AASTAQSPGMNLSHSASSLSLQQAFS------------------ELRRAQM----TEGPNT 1321

Qy   1051 TKPDRD------------------------IELELSALDTDEPDGQSEPIEEILD--IQLGISSQNDQ 1092
          ||||||                        :|
Db   1322 APPNFSHTGTPFVVPPFLSSIAGVPTTAAATAPVPATSSPPNDISTSVIQSEVTVPTEE 1381

Qy   1093 LLNGMAVENGHPVQOHQKEPPRKOKKQSLGEBDHVILEEQKTILPVTSCFSQPLPVSISNAS 1152
          |||
Db   1382 GIAGVATSTGVVTSGGLPIPP-----------------VSESPVLSSVVSSITIPAVVSISTTS 1428

Qy   1153 -CLPITTSVS 1161
           ::|
Db   1429 PSLQVPTSTS 1438
```

RESULT 12
US-10-010-720-2
Sequence 2, Application US/10010720
Patent No. 6858419
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Hansen, Gwenn
APPLICANT: Beltrandelrio, Hector
APPLICANT: Van Sligtenhorst, Isaac
TITLE OF INVENTION: No. 6858419e1 Human Kinases and Polynucleotides
TITLE OF INVENTION: Encoding the Same, And Uses Thereof
FILE REFERENCE: LEX-0382-USA
CURRENT APPLICATION NUMBER: US/10/010,720
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/206,015
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/854,856
PRIOR FILING DATE: 2000-05-14
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 2382
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(2382)
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-2

Query Match   3.1%; Score 194; DB 2; Length 2382;
Best Local Similarity 18.5%; Pred. No. 1.2e-05;
Matches 235; Conservative 167; Mismatches 506; Indels 362; Gaps 49;

```
Qy    48 KACPFDQTAINT------------------DIDVLPVNFALLQLVGAQVPDHQSIKLSNLGEN 92
Db   375 KRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLEMATSEYP------------ 421

Qy    93 KHYEVAKKCVEDLALYLKPLSGGKGVASLNQSAL----------SRPMQRKLVTLVN 139
Db   422 -----YSEQNAAQIYPRVTSGVK-PASFDKVAIPEVKEIIEGCIRQNKDERYSIKDLLN 475

Qy   140 CQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANLWAAVRARGCQFLGPAMQEE 199
Db   476 HAFFQEETGVRVELAEEDDGEKIAIKLWLRIEDIKKLK-----------GKYKDNE 520

Qy   200 ALKLVLILALEDGSALSRKVLVLFVVQRLEPRPPQASKTSIGHVVQLLYRASCPKVTKRDE 259
Db   521 AIEF------------------SFDLERDVPEDVAQEMVESGYVCEGDHKTMAKAIKDR-- 561

Qy   260 DSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLAHKSHMQSIID 319
Db   562 -VSLIKRKEQR--QLVREEQEKK------------KQEESSLKQVEQSSASQTGIK 604

Qy   320 KLQSPESFAKSVQELTIVLQRTGDP----------ANLNRLRPHLELLANIDPNPDAVSPTW 371
Db   605 QLPSASTGIPTASTTSASVSTQVEPEPEEADOHQQLQYQOPSISVLS--DGTVDSGQGSS 662

Qy   372 EQLENAMVAVKTVVHGLVDFIQNYSRKGHET----------POPQPNSKYKTSMCRDL 419
Db   663 VFTESRVSSQQTVSYG-----------SQHEQAHSTGTVPGHIPSTVQAQSQPHGVVPPSSVAQG 716

Qy   420 RQQGGCPRGTNCTFAHSQEELEXYRLRNKKINATVRTFPLLNKVGVANNTVTTTAGNVISV 479
Db   717 QSGGQ-PSSSLTGVSSSQQPIQHPQ------------QQQGIQQTAPPQ------ 752

Qy   480 IGSTETTGKIVPSTNGTNGISNAENSVSQOLISRSTDSTLRALETVKVGKVGANGQNAAGPSA 539
Db   753 -----------------------QTVQYSLSQ-TSTSSEAT-------- 779

Qy   540 DSVTENKIGSPPKTPVSNVAATSAGPSN--VGTELNSVPQKSSPFLTRV--------PVVPP 591
Db   780 PQVLP-QVSAGKQLPVSQPVPTIQGEPQIPVATOPSVVPVHSGAHFLPVGQPLPTPLLP- 837

Qy   592 HSENIQYFQDPRTQIPFEVPQY--PQTQYYPPPTVPAGVAPCVPRFVRSNNVPESSLP- 648
Db   838 -----------QYPVSQOIPISTPHVSTAQTGFSSLPITMAAGITQ--PLLTLASSATTAAIPG 887

Qy   649 -----PASMPYADHYSTFSPRDRMNSSPY----------QPPP------POPYGPVPPVPSGGMYAPV 694
Db   888 VSTVVPSQLP-----------TLLQPVTQLPSQVHPQLLQPAVQSMGIPANLGQOAAAEVPLSSGGDVL 942

Qy   695 YDSRRIWRPPMYQRDDIIRSNSLPPMDVNHSSSVYQTSLRERYNSLDGYYSVSVACQPPSEPR 754
Db   943 YQGFPPPRLPPQYPGDSNIAPSSNVASVCIHSTVLXPPMPTEVLATPGYFPPTVVQPYVESN 1002

Qy   755 TTVPL-----------PREPCGHL----KTSCEEQIRRKPDQWAQYHTQKAPLVSSTLPVATQ 802
Db  1003 LLIVPMGGVGGQVOVSQPGGSLAQAPTTSSQQAVLES--------TQGYSQVAPAEPVAVA 1054

Qy   803 SP--TPPSPL-FSVDF----------RADFSESVSGTKFEEDHLSHYSPWSCGTIGSCINAI 851
Db  1055 QPQATQPTTLASSVDSAHSDVASGMSDGNVENVPSSSGRHEGRTTKRHYRKSVRSRHEK 1114

Qy   852 DSSEPKDVIAN------SNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIPIPPFSDGPIISKWG 906
Db  1115 TSRPKLRILNVSNKGDRVVECQLETHNRKMVTFKFDLGDGNPEEIATIMVVNNDFIL--- 1170

Qy   907 AIRSS-----------------RTGYHTTDPVQA--------TASQ---GSATKP 934
Db  1171 AIERESFVDQVREIIEKADEMLSEDVSVEPEOGDQGLESLQGKDDIYGFSGSSQKLEGEFKQP 1230

Qy   935 ISVSDYVPYVNAVDSRWSSYGNEATSSAHYVERDRFIVTDLSGHRKHSS---TGDLL-SL 990
Db  1231 IPASSMPQOIGIPTS-------SLTQVVHSAGR-RFIVSPVPESRLRESKVFPSSEITDTV 1282

Qy   991 ELCQOAKSNSLLLQREANALLAMOQKWNSLDEGRHLITLNLLSKEIELRNGELQSDVTEDATD 1050
Db  1283 AASTAQSPGMNLSHSASSLSLOQAFS----------ELRRAQM--TEGPNT 1321

Qy  1051 TKPDRD-----------IELELSALDTDEPDGQOSEPIEEILD--IQLGISSQNDQ 1092
Db  1322 APPNFSHTGPTFPVVPPFLSSIAGVPTTAAATAEPVPATSSPPNDISTSVVIQSEVTVPTEE 1381

Qy  1093 LLNGMAVENGHPVQOHOQKEPPKQKKQSLGEDHVILEBQKTILPVTTSCFSQOPLPVSISNAS 1152
Db  1382 GIAGVATSTGVVTSGGLPIPP-----------VSESPVLSSSVVSSIITPAVVSISTTS 1428

Qy  1153 -CLPITTSVS 1161
Db  1429 PSLQVPTSTS 1438
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RESULT 13
US-09-854-856-48
Sequence 48, Application US/09854856
Patent No. 6541252
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Hilbun, Erin
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. 6541252e1 Human Kinases and Polynucleotides
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0178-USA
CURRENT APPLICATION NUMBER: US/09/854,856
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 60/206,015
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 1939

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;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(1939)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-48

Query Match    3.1%;  Score 193.5;  DB 2;  Length 1939;
Best Local Similarity  19.2%;  Pred. No. 9e-06;
Matches 256;  Conservative 168;  Mismatches 527;  Indels 379;  Gaps 57;

Qy    114  GGKGVASLNQSALSRPMQRKLVTLVNCQLVEEGRVR-AMRAARSLGERTVTELILQHQN  172
Db    660  GQPSSSSLTGVSSSQPIQHPQQQQGIQQTAPPQQTVQYSLSQSTSSSEATTAQPVSQPQA 719

Qy    173  PQQLSANLWAAVRARGCQPLGPA-----MQEEALKLVLLALEDGSALSRKVLVLFVVQRL  227
Db    720  PQVLPQVSAGKQSTQGVSQVQVAPAEPVAVAQPQATQPTTLASSVDSAHSD--VASGMSDG 776

Qy    228  EPRFPQQASKTISIGHVVQLLYRASCFKVTKRDEDSSLMQLK------EEFRSYEALRREHD 281
Db    777  NENVPSSGRHEGRTTKRHYRKS-VRSRSRHEKTSRPKLRILNVSNKGDRVECQLETHN   835

Qy    282  AQIVHIAMEAGLRISPEQWSSLLY-GDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQR  340
Db    836  RKMVTFKPDLD-GDNPEEIATIMVNNDPILAIERESFVDQVREIIEKADEMLSEDVSVEP  894

Qy    341  TGDPANLNRLRPHLELLANID------PNPDAVSPTWEQLENAMVAVKTV            384
Db    895  EGDQG------LESLQGKDDYGFSGSGSQQKLEGEFKQPIPASSMP--QOIGIPTSSLTQV 944

Qy    385  VHGLVDFIQNYSRKGHETPQPQN------SKYKTSMCRDLRQQGGCPRGTNCTFAHS     436
Db    945  VH------SAGRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPG------MNLSHS    991

Qy    437  QEELEKYR----LRNKKI------NATVRTFP-------LLNKVGVNNTVTVTTA--     473
Db    992  ASSLSLQQAFSELRRAQMTEGPNTAPPNFSHTGPTFPVVPPFLSSIAGVPTTAAATAPVP 1051

Qy    474  ------GNVISVIGSTETTGKIVPSTNGISNAENS-------VSQLIS             508
Db   1052  ATSSPENDISTSVIQSEVT--VPTEEGIAGVATSTGVVTSGGLPIPPVSESPVLSSVVS  1108

Qy    509  RSTDSTLIRALETVTKKVSKVGAN------GQNAAGPSAD-SVTENKIG-----SPPKTPVSN 557
Db   1109  SITIPAVVSISTTSPSLQVPTSEIVVSSTALYPSVTVSATSASAGGSTATFPGPKPPAV  1168

Qy    558  VAATSAGPSNVGTELNSV-------PQKSSPFLTRVPVPPHSENIQYF            599
Db   1169  VSQQAAGSTTVGATLTSVSTTTSFPSTASQLSTQLSSSTSTPTLAEFTVVVSAHSLD-KTS 1227

Qy    600  QDPRTQIPFEVPQYPQTGYYPPPP-------TVPAGVAPCV-PRFVRSNNVPESSLPPASMP 653
Db   1228  HSSTTGLAFSL-SAPSSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTP 1286

Qy    654  YADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPVPSGM------YAPVYDS          697
Db   1287  L------LPQVPSIPPLVQPVANVPAVQQTLIHSQPQPALLPNQPHTHCPEVDS       1334

Qy    698  RRIWRPPMYQRDDI------IRS--NSLPPMDVMHSSV-YQTSLRERYNSLDGYYSVA-  746
Db   1335  DT--QPKAPGIDIKTLEEKLRSLFSEHSSSSGAQHASVSLIETSLVIESTVTPGIPTTAVA 1392

Qy    747  ------CQPPSE-PRTTVPLRPEPC-----GHLKTSCEEQIRR-KPDQWAQYHTQKA    790
Db   1393  PSKLLITSTTSTCLPPINLPLGTVALPVTPVVTPGQVSTPVSTTNSGVKPGT---APSKP 1448

Qy    791  PLVSS-TLPVATQSPTTPPSLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCCTIGSCIN 849
Db   1449  PLTKAPVLPVGTELP------------------------------AGTLPS--E     1470

Qy    850  AIDSEPKDVIANSNAVLMDLDS--------------------GDVKRRVHLFETQRRTK--- 888
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RESULT 14
US-10-010-720-48
; Sequence 48, Application US/10010720
; Patent No. 6858419
; GENERAL INFORMATION:
;   APPLICANT: Walke, D. Wade
;   APPLICANT: Hilbun, Erin
;   APPLICANT: Donoho, Gregory
;   APPLICANT: Turner, C. Alexander Jr.
;   APPLICANT: Hansen, Gwenn
;   APPLICANT: BeltrandelRio, Hector
;   APPLICANT: Van Sligtenhorst, Isaac
;   TITLE OF INVENTION: No. 6858419e1 Human Kinases and Polynucleotides
;   TITLE OF INVENTION: Encoding the Same, And Uses Thereof
;   FILE REFERENCE: LEX-0382-USA
;   CURRENT APPLICATION NUMBER: US/10/010,720
;   CURRENT FILING DATE: 2002-05-21
;   PRIOR APPLICATION NUMBER: US 60/206,015
;   PRIOR FILING DATE: 2000-05-19
;   PRIOR APPLICATION NUMBER: US 09/854,856
;   PRIOR FILING DATE: 2000-05-14
;   NUMBER OF SEQ ID NOS: 64
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 1939
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(1939)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-10-010-720-48

Query Match    3.1%;  Score 193.5;  DB 2;  Length 1939;
Best Local Similarity  19.2%;  Pred. No. 9e-06;
Matches 256;  Conservative 168;  Mismatches 527;  Indels 379;  Gaps 57;

Db   1471  QLPPFGPSLTQSQQPLEDLDAQLRRTLSPEXITVTSAVGPVSMAAPTAITEAGTQPQKG  1530
Db   1591  SSSPESTLVKPEPNGITIPGISSDVPESAHKTTASEAKSDTGQPTKVGRRFQVTTANKVG  1650
Db    889  -----EEDIIPFSDGPIISKWG----AISRSRRTGYHTTDPVQATASQGSATKPISVS    938
Qy    939  DYVPVVNAV-----------DSRWSSYGNEATS-SAHVVERDRFIVTDLS---G        977
Db   1531  VSQVKEGPVLATSSGAGVPFKMGRFQVSVAADGAQKEGKNKSEDAKSVHFESSTSESSVLS 1590
Db    978  HRKHSSTGDLLS--------LELCQAKSNSLLLQREANALLAMQQKWN------      1016
Db   1651  RFSVSKTEDKITDTKKEEGPVASPPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPSSDPEA 1710
Db   1017  -------SLDEGR--HLTLNLLSKEIELRN-----GELQSDY-TEDATDTKPDDIELEL   1061
Db   1711  AFLSRDVDDGSGSPHSPHQLSSKSLPSQNLSQSLSNSFNSSYMSSDNESDIEDEDLKLEL  1770
Db   1062  SALDTDEPDGQSEPIEEILIDIQLGISSQNDQLLN-----GMAVENGHPVQQHQKEPPK   1114
Db   1771  RRL------RDKHLKEIQDLQSRQKHEIIESLYTKLIGKVPPAVIIPPAAPLSGRRRRPTK 1823
Qy   1115  QK------KQSLGEDH-------VILEEQKTILPVTSCFSQPLPVSISNASCLP       1155
Db   1824  SKGSKSRSSSSLGNKSPQLSGNLSGQSAASVLHPQQTLHPPGN-----IPESGQNQLLQP  1878
Qy   1156  ITTSVSAGNL                                                  1165
Db   1879  LKPSPSSDNL                                                  1888

Qy    114  GGKGVASLNQSALSRPMQRKLVTLVNCQLVEEGRVR-AMRAARSLGERTVTELILQHQN  172
Db    660  GQPSSSSLTGVSSSQPIQHPQQQQGIQQTAPPQQTVQYSLSQSTSSSEATTAQPVSQPQA 719
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```
Qy    173 PQQLSANLWAAVRARGCQFLGPA-------MQEEALKLVLLALEDGSALSRKVLVLFVVQRL 227
          |:|  |||||
Db    720 PQVLPQVSAGKQSTQSVSQVARPAEPVAVAVQPQATQPTTLASSVDSAHSD---VASGMSDG 776

Qy    228 EPRFPQASKTSIGHVVQLLYRASCFKVTKRDEDSSIMQLK--------EEFRSYEALRREHD 281
          ||| |||||||
Db    777 NENVPSSSGRHEGRTTKRHYRKS-VRSRSRHEKTSRPKLRILNVSNKGDRVVEQCLETHN 835

Qy    282 AQIVHIAMEAGLRISPEQWSSLLY-GDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQR 340
          ||||||||||||
Db    836 RKMVTFKPDLD-GDNPEEIATIMVNNDFILAIERESFVDQVREIIEKADEMLSEDVSVEP 894

Qy    341 TGDPANLNRLRPHLELLANID--------------PNPDAVSPTWEQLENAMVAVKTV 384
          ||||||||
Db    895 EGDQG-------LESLQGKDDYGFSGSGSQKLEGEFKQPIPASSMP--QOIGIPTSSLTQV 944

Qy    385 VHGLVDFIQNYSRKGHETPQPQN-------SKYKTSMCRDLRQQGGCPRGTNCTFAHS 436
          |:|  :||:
Db    945 VH----------SAGRRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPG-----MNLSHS 991

Qy    437 QEELEKYR----LRNKKI-----NATVRTFP-----LLNKVGVNNTVTTTA--- 473
          |||  |  :||
Db    992 ASSLSLQQAFSELRRAQMTEGPNTAPPNFSHTGPTFPVVPPFLSSIAGVPTTAAATAPVP 1051

Qy    474 -------GNVISVIGSTETTGKIVPSTNGISNAENS---------------VSQLIS 508
          |||
Db   1052 ATSSPPNDISTEVIQSEVT----VPTEEGIAGVATSTGVVTSGGLPIPPVSESPVLSSVVS 1108

Qy    509 RSTDSTLRALETVKKVGKVGAN-------GQNAAGPSAD-SVTENKIG---SPPKTPVSN 557
          ||  :||||
Db   1109 SITIPAVVSISTTSPSLQVPTSTSEIVVSSTALYPSYTVSASAGGSTATPGKPPAV 1168

Qy    558 VAATSAGPSNVGTELNSV-------POKSSPPLTRVPVPYPHSENIQYF 599
          |:|  ||||
Db   1169 VSQQAAGSTTVGATLTSVSTTTSFPSTASQLSLSSSTSPTPLAETVVVSAHSLD-KTS 1227

Qy    600 QDPRTQIPFEVPQYPQTGYVPPP-----TVPAGVAPCV-PRFVRSNNVPESSLPPASMP 653
          |:|  ||:|
Db   1228 HSSTTGLAFSL-SAPSSSSSPAGVSSYISQPCGLHPLVVIPSVIASTPILPQAAGPTSTP 1286

Qy    654 YADHYSTFSPRDRMNSSPYQPPPPOPYGPVPVPVPSGM-------YAPVVDS 697
          |:|  :|||||
Db   1287 L------------LPQVPSIPPLIVQPVANVPAVQQTLIHSQPOPALLPNQPHTHCPEVDS 1334

Qy    698 RRIWRPEMYQRDDI--------IRS--NSLPPMDVMHSSV-YQTSLRERYNSLDGYYSVA- 746
          ||||
Db   1335 DT--QPKAPGIDDIKTLEEKLRSLFSEHSSSGAQHASVSLETSLVIESTVTPGIPTTAVA 1392

Qy    747 ------COPPSE-PRTTVPLPREPC--GHLKTSCEQIRR-KPDQWAQYHTQKA 790
          |||  :|||
Db   1393 PSKLLTSTTSTCLPPTNLPLGTVALPVTPVVTPGQVSTPVSTTSGVKPGT----APSKP 1448

Qy    791 PLVSS-TLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCCTIGSCIN 849
          |:|  :||||
Db   1449 PLTKAPVLPVGTELP----------------------------------AGTLPS--B 1470

Qy    850 AIDSEPKDVIANSNAVLMDLDS-----------GDVKRRVHLFETQRRTK---- 888
          ||||
Db   1471 QLPPFPGPSLTQSQQPLEDLDAQLRRTLSPEXITVTSAVGPVSMAAPTAITEAGTQPQKG 1530

Qy    889 ----EEDPIIPSDGPIISKWG------AISRSSRTGYHTTDDVQATASQGSATKPISVS 938
          ||
Db   1531 VSQVKEGPVLATSSGAGVPKMGRPQVSVAADGAOKEGHQNKSEDAKSVHFESSTSESSVLS 1590

Qy    939 DVYPYVNAV-------DSRWSSYGNEATS-SAHYVERDRFIVTDLS--G 977
          |:|  |||
Db   1591 SSSPESTLVKPPNGITIPGISSDVPESAHKTTASEAKSDTGQPTKYGRFQVTTANKVG 1650

Qy    978 HRKHSSTGDLLS----------LELQQAKSNSLLLQREANALAMOOKWN------- 1016
          |:|  ||
Db   1651 RFSVSKTEDKITDTKKEGPVASPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPSSDPEA 1710

Qy   1017 -----SLDEGR--HLTLNLLSKEIELRN-------GELQSDY-TEDATDTKPDRDIELEL 1061
          ||
Db   1651 RFSVSKTEDKITDTKKEGPVASPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPSSDPEA 1710
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RESULT 15
US-09-854-856-16
; Sequence 16, Application US/09854856
; Patent No. 6541252
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hillbun, Erin
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 654125201 Human Kinases and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0178-USA
; CURRENT APPLICATION NUMBER: US/09/854,856
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/206,015
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1999
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1999)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-854-856-16

Query Match 3.1%; Score 193.5; DB 2; Length 1999;
Best Local Similarity 19.2%; Score Pred. No. 9.5e-06;
Matches 256; Conservative 168; Mismatches 527; Indels 379; Gaps 57;

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Qy    114 GGKGVASLNQSALSRPMQRKLVTLVNCQLVEEGRVR-AMRAARSLGERTVTELILQHQN 172
          |:|  :|||
Db   1062 SALDTDEPDGQSEPIEEILDIQLGISSQNDQLLN-------GMAVENGHPVQOHQKEPPK 1114

Qy    173 PQQLSANLWAAVRARGCQFLGPA----MQEEALKLVLLALEDGSALSRKVLVLFVVQRL 227
          |:|  :|||||
Db   1823 RDKHLKEIQDLQSRQKHEIESLYTKLGKVPPAVIIPPAAPLSGRRRRPTK 1770

Qy    228 EPRFPQASKTSIGHVVQLLYRASCFKVTKRDEDSSIMQLK-----EEFRSYEALRREHD 281
          ||| |||||||
Db    837 NENVPSSSGRHEGRTTKRHYRKS-VRSRSRHEKTSRPKLRILNVSNKGDRVVEQCLETHN 895

Qy    282 AQIVHIAMEAGLRISPEQWSSLLY-GDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQR 340
          |||  ||||||||
Db    896 RKMVTFKPDLD-GDNPEEIATIMVNNDFILAIERESFVDQVREIIEKADEMLSEDVSVEP 954

Qy    341 TGDPANLNRLRPHLELLANID-----------PNPDAVSPTWEQLENAMVAVKTV 384
          ||||||||
Db    955 EGDQG-------LESLQGKDDYGFSGSGSQKLEGEFKQPIPASSMP--QOIGIPTSSLTQV 1004

Qy    385 VHGLVDFIQNYSRKGHETPQPQN--------SKYKTSMCRDLRQQGGCPRGTNCTFAHS 436
          |:|  :||:
Db   1005 VH----------SAGRRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPG-----MNLSHS 1051

Qy    437 QEELEKYR----LRNKKI-----NATVRTFP-----LLNKVGVNNTVTTTA-- 473
          |||  |
Db   1051
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Db   1052  ASSLSLQQAFSELRRAQMTBGPNTAPPNFSHTGPTFPVVPPFLSSLAGVPTTAAATAPVP  1111
                ||:             :::        ||||                   :|| :|
Qy    474  -----GNVISVIGSTETTGKIVPSTNGISNAENS----------------------VSQLIS   508

Db   1112  ATSSPPNDISTSVIQSEVT---VPTEEGIAGVATSTGVVTSGGLPIPPVSESSPVLSSVVS  1168
                :::|:|       ||:     |      |:|                   :::
Qy    509  RSTDSTLRALETVKKVGKVGAN------GQNAAGPSAD-SVTENKIG-----SPPKTPVSN   557

Db   1169  SITIPAVVSISTTSPSLQVPTSTSEIVVSSTALYPSVTVSATSASAGGSTATPGKPPAV  1228
                :  :   :   :|||                            :|:
Qy    558  VAATSAGPSNVGTELNSV---------------------PQKSSPFLTRVPVYPPHSENIQYF   599

Db   1229  VSQQAAGSTTVGATLTSVSTTTSFPSTASQLSIQLSSSTSTPTLAETVVVSAHSLD-KTS  1287
                 :    |||
Qy    600  QDPRTQIPFEVPQYPQTGYYPPPP-------TVPAGVAPCV-PRFVRSNNVPESSLPPASMP   653

Db   1288  HSSTTGLAFSL-SAPSSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTP  1346
                :       |||
Qy    654  YADHYSTFSPRDRMNSSPYQPPPPQPYGPVPPVPSGM-------------YAPVYDS   697

Db   1347  L------------LPQVPSIPPLVQPVANVPAVQQTLIHSQPQPALLPNQPHTHCPEVDS  1394
                |                |||
Qy    698  RRIWRPPMYQRDDI-------IRS--NSLPPMDVMHSSV-YQTSLRERYNSLDGYYSVA--   746

Db   1395  DT--QPKAPGIDDIKTLEEKLRSLFSEHSSSGAQHASVSLETSLVIESTVTPGIPTTAVA  1452
                :                       |||
Qy    747  --------COPPSE-PRTTVPLPREPC---GHLKTSCEEQIRR-KPDQWAQYHTQKA   790

Db   1453  PSKLLTSTTSTCLPPTNLPLGTVALPVTPVVTPGQVSTPVSTTTSGVKPGT----APSKP  1508
                |||                            |||
Qy    791  PLVSS-TLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSCIN   849

Db   1509  PLTKAPVLPVGTELP---------------------------------AGTLPS--E  1530
                |||
Qy    850  AIDSEPKDVIANSNAVLMDLDS------------------GDVKRRVHLFETQRRTK----   888

Db   1531  QLPPPPGPSLTQSQQPLEDLDAQLRRTLSPEKITVTSAVGPVSMAAPTAITEAGTQPQKG  1590
                :                                :||
Qy    889  ---EEDPIIPPSDGPIISKWG-----AISRSSRTGYHTTDPVQATASQGSAATKPIISVS   938

Db   1591  VSQVKEGPVLATSSGAGVFKMGRFQVSVAADGAQKEGKNKSEDAKSVHFESSTSESSVLS  1650
                :|||
Qy    939  DYVPYVNAV----------DSRWSSYGNEATS-SAHYVERDRFIVTDLS---G   977

Db   1651  SSSPESTLVKPEPNGITIPGISSDVPESAHKTTASEAKSDTGQPTKVGRFQVTTTANKVG  1710
                ::||
Qy    978  HRKHSSTGDLLS---------LELQQAKSNSLLLQREANALAMQQKWN-------  1016

Db   1711  RFSVSRKTEDKITDTKKEGPVASPPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPSSDPEA  1770
                ::|
Qy   1017  -----SLDEGR--HLTLNLLSKEIELRN-------GELQSDY-TEDATDTKPDRDIELEL  1061

Db   1771  AFLSRDVDDGGSGSPHSPHQLSKSKLPSQNLSGOSLSNSFNSSVTMSSDNESDIEDEDLKUEL  1830
                ::|   ||:::|:|||:::
Qy   1062  SALDTDEPDGQSEPIEEILDIQLGISSQNDQLLN--------GMAVENGHPVQOHQKEPPK  1114

Db   1831  RRL-------RDKHLKEIQDLQSRQKHEIESLYTKLGKVPPAVIIPPAAPLSGRRRRPTK  1883
                ||:                   ::|
Qy   1115  QK-------KOSLGBDH--------VILEBQKTILPVTSCFSQPLPVSISNASCLP  1155

Db   1884  SKGSKSSRSSLGNKSPOLSGNLSGQSAAASVLHPQQTLHPQGN-----IPESGQNOLLQP  1938
                :|||                   |:|:|:|
Qy   1156  ITTTSVSAGNL  1165

Db   1939  LKPSPSSDNL  1948
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OM protein - protein search, using sw model

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                        GenCore version 5.1.8
                        Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on:                 May 24, 2006, 12:51:25 ; Search time 112 Seconds
                                          4925.794 Million cell updates/sec
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Title:                  US-10-619-992-2
Perfect score:          6215
Sequence:               1 MPVQAAQWTEFLSCPICYNE.........MSEDKNDFLKPVANGKMVNS 1191

Scoring table:          BLOSUM62
                        Gapop 10.0 , Gapext 0.5

Searched:               2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:    2097797

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :        Published Applications_AA Main:*
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           2: /EMC_Celera_SID3/ptcdata/2/pubpaa/US08_PUBCOMB.pep:*
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           6: /EMC_Celera_SID3/ptcdata/2/pubpaa/US11_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	6215	100.0	1191	3	US-09-921-099-2	Sequence 2, Appli
2	6215	100.0	1191	5	US-10-619-992-2	Sequence 2, Appli
3	6207	99.9	1191	3	US-09-921-099-4	Sequence 4, Appli
4	6207	99.9	1191	5	US-10-619-992-4	Sequence 4, Appli
5	5483	88.2	1048	5	US-10-485-225-8	Sequence 8, Appli
6	1538	24.7	819	6	US-11-097-143-24915	Sequence 24915, A
7	843	13.6	1048	5	US-10-619-992-11	Sequence 11, Appl
8	611	9.8	522	4	US-10-104-047-3665	Sequence 3665, Ap
9	611	9.8	522	6	US-11-072-512-3665	Sequence 3665, Ap
10	490	7.9	95	3	US-09-867-550-1346	Sequence 1346, Ap
11	311	5.0	67	5	US-09-864-761-48290	Sequence 48290, A
12	267	4.3	276	5	US-10-450-763-41493	Sequence 41493, A
13	208	3.3	1552	5	US-10-330-773-941	Sequence 941, App
14	207	3.3	2377	5	US-10-840-512-196	Sequence 196, App
15	203	3.3	674	6	US-11-096-568A-27756	Sequence 27756, A
16	203	3.3	786	6	US-11-096-568A-27755	Sequence 27755, A
17	203	3.3	1267	4	US-10-092-900A-128	Sequence 128, App
18	200.5	3.2	728	5	US-10-732-923-6679	Sequence 6679, Ap
19	200	3.2	639	6	US-11-096-568A-27757	Sequence 27757, A
20	198.5	3.2	3586	6	US-11-034-143-77	Sequence 77, Appl
21	196.5	3.2	1248	5	US-10-437-963-126940	Sequence 126940,
22	195.5	3.1	123	3	US-10-288-798-9	Sequence 9, Appli
23	195	3.1	2135	4	US-10-362-892-9	Sequence 9, Appli
24	195	3.1	2135	4	US-10-196-935A-2	Sequence 2, Appli
25	195	3.1	2382	4	US-10-052-648A-40	Sequence 40, Appl
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33	192.5	3.1	1756	5	US-10-240-145-145	Sequence 145, App
34	191.5	3.1	2816	4	US-10-291-128-145	Sequence 145, App
35	191.5	3.1	2816	5	US-10-840-512-119	Sequence 119, App
36	191.5	3.1	1129	5	US-10-704-781-3	Sequence 3, Appli
37	191	3.1	4262	5	US-10-704-781-4	Sequence 4, Appli
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40	190	3.1	922	4	US-10-128-7714-3473	Sequence 3473, Ap
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43	185.5	3.0	1343	4	US-10-291-128-145	Sequence 145, App
44	185.5	3.0	2325	4	US-11-098-686-11135	Sequence 11135, A
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ALIGNMENTS

RESULT 1
US-09-921-099-2
; Sequence 2, Application US/09921099
; Patent No. US2002010737201
; GENERAL INFORMATION:
; APPLICANT: Heteneider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene at
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/09/921,099
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-921-099-2

Query Match 100.0%; Score 6215; DB 3; Length 1191;
Best Local Similarity 100.0%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1191;

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; SEQ ID NO 2
;   LENGTH: 1191
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-619-992-2

Query Match 100.0%; Score 6215; DB 5; Length 1191;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Left column (RESULT 3)

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RESULT 3
US-09-921-099-4
Sequence 4, Application US/09921099
Patent No. US20020107372A1
GENERAL INFORMATION:
;  APPLICANT: Hefeneider, Steven
;  APPLICANT: Merkins, Louise
;  APPLICANT: Bennett, Robert
;  APPLICANT: Seiss, Donald
;  TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene a
;  FILE REFERENCE: 00-617-A
;  CURRENT APPLICATION NUMBER: US/09/921,099
;  CURRENT FILING DATE: 2001-08-01
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: Patentin version 3.0
;  SEQ ID NO 4
;  LENGTH: 1191
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-921-099-4

Query Match             99.9%;
Best Local Similarity   99.9%;
Matches 1190; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Score 6207;  DB 3;  Length 1191;
Pred. No. 0;

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Right column (RESULT 4)

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RESULT 4
US-10-619-992-4
Sequence 4, Application US/10619992
Publication No. US2005023916381A1
GENERAL INFORMATION:
;  APPLICANT: Hefeneider, Steven
;  APPLICANT: Merkins, Louise
;  APPLICANT: Bennett, Robert
;  APPLICANT: Seiss, Donald
;  TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene ar
;  FILE REFERENCE: 00-617-A
;  CURRENT APPLICATION NUMBER: US/10/619,992
;  CURRENT FILING DATE: 2003-07-15
;  PRIOR APPLICATION NUMBER: US/09/921,099
;  PRIOR FILING DATE: 2001-08-01
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: Patentin version 3.0
;  SEQ ID NO 4
;  LENGTH: 1191
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-619-992-4

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Db  901 IISKWGAISRSRSRTGYHTTDPVQATASQSSATKPISVSDYVPYVNAVDSRWSSYGNEATS 960

Qy  901 IISKWGAISRSRSRTGYHTTDPVQATASQSSATKPISVSDYVPYVNAVDSRWSSYGNEATS 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE 1020

Qy  961 SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL 1080

Qy 1021 GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 DIQLGISSQNDQLLNGMAVENGHPVQOHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCF 1140

Qy 1081 DIQLGISSQNDQLLNGMAVENGHPVQOHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCF 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 SQPLPVSISNASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGRKMVNS 1191

Qy 1141 SQPLPVSISNASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGRKMVNS 1191
         |||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Query Match    99.9%;  Score 6207;  DB 5;  Length 1191;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 1190;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy     1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MAVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTD 60

Qy    61 IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVAS 120

Qy   121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANL 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANL 180

Qy   181 WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240

Qy   241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300

Qy   301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360

Qy   361 DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLR 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLR 420

Qy   421 QQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTAGNVISVI 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 QQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTAGNVISVI 480

Qy   481 GSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGONAAGPSAD 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGONAAGPSAD 540

Qy   541 SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPPHSENIQYFQ 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPPHSENIQYFQ 600

Qy   601 DPRTQIPFEVPQYPQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 DPRTQIPFEVPQYPQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660

Qy   661 FSPRDRMNSSPYQPPPPQPYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 FSPRDRMNSSPYQPPPPQPYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM 720

Qy   721 DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD 780

Qy   781 QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS 840

Qy   841 CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRVHLFETQRRTKEEDPIIPFSDGP 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRVHLFETQRRTKEEDPIIPFSDGP 900

Qy   901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPVNAVDSRWSSYGNEATS 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPVNAVDSRWSSYGNEATS 960

Qy   961 SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLQREANALAMQQKWNSLDE 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLQREANALAMQQKWNSLDE 1020
```

```
Query Match    88.2%;  Score 5483;  DB 5;  Length 1048;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1048;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTD 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTD 60

Qy    61 IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVAS 120

Qy   121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANL 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANL 180

Qy   181 WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240

Qy   241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300

Qy   301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360

Qy   361 DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLR 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLR 420

Qy   421 QQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTAGNVISVI 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 QQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTAGNVISVI 480
```

Continuation of first alignment (Query Match 99.9%):

```
Qy  1021 GRHITLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSRPIEEIL 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GRHITLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSRPIEEIL 1080

Qy  1081 DIQLGISSQONDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCF 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 DIQLGISSQONDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCF 1140

Qy  1141 SQPLPVSISNASCLPITTSVSAGNILKTHVMSEDKNDFLKPVANGKMVNS 1191
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 SQPLPVSISNASCLPITTSVSAGNILKTHVMSEDKNDFLKPVANGKMVNS 1191
```

```
;
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 24915
; LENGTH: 819
; TYPE: PRT
; ORGANISM: DROSOPHILA
;
US-11-097-143-24915

  Query Match             24.7%;  Score 1538;  DB 6;  Length 819;
  Best Local Similarity   40.5%;  Pred. No. 2.1e-97;
  Matches   386;  Conservative  98;  Mismatches  226;  Indels 242;  Gaps  29;

Qy      1 MPVQAAQWTEFLSCPICVNEFDENVHKPISLGCGHTVCKTCLNKLHRKACPFDQTAINTD 60
          ||| :|   | :: |||||   :|| |:||:   | :|||:|| ||:|:|||||||| ::|
Db      1 MPIQAPSWTDFLNCPICCNEFASQRCPVSLGCGHTICKLCLTTLYNRQCPFDQTVIVSD 60

Qy     61 IDVLPVNFALLQLV----------GAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPL 112
          || :|:|| ||||:          |  ||||| :||:||||||||| ||||||:|||| ||
Db     61 IDNLPINHALLQLVKDSELLELAPPPSVQKLEPEHL---KCYQLGQRCTEELALHLKSF 117

Qy    113 SGGKGVASLNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQN 172
          :| |||:||||:|:||| |||||||||||||||||||||||||||||||||||||||||:
Db    118 LNLNG----NGNLLTRPMLRKLVTLVNCQLMEEEGRVRALRAARSLGERTVTELILQHQN 173

Qy    173 PQQLSANLWAAVRARGCQFLGPAMQEEALKLVTLLALEDGSALSRKVLVLFVVQRLEPRFP 232
          |||:| ||||||:|||||||||||||||:||||||||||||||||:|||:|||||||||:
Db    174 PQQLSSNLWAAVRTRGCQFLGPAMQEEVLKLVLLALEBGSALSRKVLVMFVVQRLEPKFP 233

Qy    233 QASKTSIGHVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALLRREHDAQIVHIAMEAG 292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    234 QASKTSIGHVVQLLYRASCFKVSKREADSSLMQLKEEFRTYDALRREHDAQIVQIATEAG 293

Qy    293 LRISPEQWSSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANINRLRP 352
          ||| ||||||||| | :|||||||||| | :|||  | :|||:|| |||:|||| |: |
Db    294 LRIAPEQWSSLLYGDVMHKSHMQSIIDKLQTPSSFAQSVQELVIALQRTSDPAKLSSLHH 353

Qy    353 HLELLANIDPNPDAVSPTWEQLENAMVAYKTVVHGLVDFIQNYS--RK------GHETPQ 404
          ||: |||||||||||||:||||||  : | :| :|| |: || :  ::       |: |
Db    354 HLKYLANIDPCAE-VAP-WSVLAEALDAVAHSVGLVNFLQHHGVRKAQDGISGGGSGGT 411

Qy    405 PQPNSKYKTSMCRDLRQQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVG 464
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    412 TNSNPKYKLSLCRDLNVRRVCPRGSSCTFAHSQEEVRYRARNR------------- 455

Qy    465 VNNNTVTTAGNVISVIGSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKV 524
          : |||||||||| ||| || |||||||||||||||||||||||||||||||||||||||
Db    456 ------------------------GKHMKTPLA----LQGPPAVGAIKPLGEGEGPP 487

Qy    525 GKVGANGQNAAGPSADSVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVP--QKSSPF 582
                                    :|
Db    488 LGNMPPMLPMSP-MHYMGSPR------GYLDP--- -SLGLSP----GGGL 522

Qy    583 LTRVPVYPPHSENIQYFQODPRTQIPFEVPQYPQTGYYPPPTVPAGVAPCVPRFVRSNNV 642
          |:||| |||| | |||: ||||: |||||| |  ||:|||||||||||||||||| || |
Db    523 PPSHHSPITRLIVPSRYDSRFSGFGGGTPR------- IPSPREYQANPVAP--- 566

Qy    643 PESSLPPAS---MP--YADHYST----SPRDRMNSSPYQPPPPQPYGPVPPVSGMYAPV 694
          |:||||||:   | |  | ||:|:    :|||||||||||| |||||||||||||||| |
Db    567 --TORNANPNFSVNSNLHKGYMLPASGGDVFHLA----------NPWEQAYLAQQHPP 614

Qy    695 YDSRRIWRPPMYQRDDIIRSNSLPPM----DVMHSSVYQTSLRERYNSLDGYYSVACQPP- 750
          |||||||||||||||||||||||||     :|| || |  :|  | |:| : :
Db    615 QHPQOQQPPSSKPNPSRPLSILPAFADTSFFEKKPPNSVSIDLDRVPEVNVDAVPLFRRS 674

Qy    751 ----SEPRTTVPLPREPCGHLKTSCEEQ-IRRKPDQWAQYHTQKAPLYS-STLPVATQS 803
              :|| |||| |||| :  :|:|||||  ||||||   |: |:|| :     |||:
Db    675 --------NNNHNNNSNSHNNNNNNNHGSSLFLWN-NTGKDSANFVRS---DSILDDD 720

Qy    804 PTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSCINAIDSEPKDVIANSN 863
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db    721 PTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSCINAIDSEPKDVIANSN 780

Qy    864 AVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGPIISKWGAISRSSRTG 915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    864 AVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGPIISKWGAISRSSRTG 915
```

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RESULT 6
US-11-097-143-24915
Sequence 24915, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
  APPLICANT: Venter, J. Craig
  APPLICANT: et al.
  TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
  TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
  TITLE OF INVENTION: DROSOPHILA GENES.
  FILE REFERENCE: CL000728
  CURRENT APPLICATION NUMBER: US/11/097,143
  CURRENT FILING DATE: 2005-04-04
  PRIOR APPLICATION NUMBER: 60/157,832
  PRIOR FILING DATE: 1999-10-05
  PRIOR APPLICATION NUMBER: 60/160,191
  PRIOR FILING DATE: 1999-10-19
  PRIOR APPLICATION NUMBER: 60/161,932
  PRIOR FILING DATE: 1999-10-28
  PRIOR APPLICATION NUMBER: 60/164,769
  PRIOR FILING DATE: 1999-11-12
  PRIOR APPLICATION NUMBER: 60/173,383
  PRIOR FILING DATE: 1999-12-28
  PRIOR APPLICATION NUMBER: 60/175,693
  PRIOR FILING DATE: 2000-01-12
  PRIOR APPLICATION NUMBER: 60/184,831
  PRIOR FILING DATE: 2000-02-24
  PRIOR APPLICATION NUMBER: 60/191,637
  PRIOR FILING DATE: 2000-03-23
  NUMBER OF SEQ ID NOS: 43008
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Db    421 QQCGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNNTVTTTAGNVISVI 480

Qy    481 GSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSAD 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSAD 540

Qy    541 SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLITRVPVYPPHSENIQYFQ 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLITRVPVYPPHSENIQYFQ 600

Qy    601 DPRTQIPFEVPQYPQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 DPRTQIPFEVPQYPQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660

Qy    661 FSPRDRMNSSPYQPPPPQPYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 FSPRDRMNSSPYQPPPPQPYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM 720

Qy    721 DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD 780

Qy    781 QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS 840

Qy    841 CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP 900

Qy    901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDVYPVNAVDSRWSSYGNEATS 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDVYPVNAVDSRWSSYGNEATS 960

Qy    961 SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLQREANALAMQQKWNSLDE 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLQREANALAMQQKWNSLDE 1020

Qy   1021 GRHLTLNLLSKEIELRNGELQSDYTEDA 1048
          ||||||||||||||||||||||||||||
Db   1021 GRHLTLNLLSKEIELRNGELQSDYTEDA 1048
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Db     721 ASTFDVPTGSSMLSIY-----------------------GPICPK-------SSTTG 747


RESULT 7
US-10-619-992-11
; Sequence 11, Application US/10619992
; Publication No. US20050023163A1
; GENERAL INFORMATION:
;   APPLICANT: Hefeneider, Steven
;   APPLICANT: Merkins, Louise
;   APPLICANT: Bennett, Robert
;   APPLICANT: Seiss, Donald
;   TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene a
;   FILE REFERENCE: 00-617-A
;   CURRENT APPLICATION NUMBER: US 10/619,992
;   CURRENT FILING DATE: 2003-07-15
;   PRIOR APPLICATION NUMBER: US/09/921,099
;   PRIOR FILING DATE: 2001-08-01
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: Patentin version 3.0
;   SEQ ID NO 11
;   LENGTH: 1048
;   TYPE: PRT
;   ORGANISM: Caenorhabditis elegans
US-10-619-992-11

Query Match             13.6%;  Score 843;  DB 5;  Length 1048;
Best Local Similarity   30.6%;  Pred. No. 5.4e-49;
Matches  238;  Conservative  99;  Mismatches 278;  Indels 162;  Gaps  23;

Qy     4 QAAQWTEFLSCPICYNEEDENVHKPISLGCSHTVCKTCLNKLHR--KACPFDQTAINTDI 61
Db     6 QGCGWQEVLCCSICNRHFNE-TFLPVSLICGHVICRKCCAAEKPENQTKPCPHDDWKTIHSP 64

Qy    62 DVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVASL 121
Db    65 SEYPNNVALLSVI---FPRKQCMTLSGAVSEAEKRVDQLSIQ-IAKFFREADSERG-GTV 119

Qy   122 NQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANLW 181
Db   120 SSREISRTLQRKVLALLCYQWREVDGRLIKTLKMCRGISERVMIEILSIQSNTHVSSQLM 179

Qy   182 AAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVIVLFVVQRLREPRFPPQASKTSIGH 241
Db   180 SAVRARGCQFLGPAMQDDVLRLIMTLFTGECIARKNLVMYVVQTLASDYPQVSKTCVGH 239

Qy   242 VVQLLYRASCFKVTKRDDDSSLMQLKEEFRSYEALRREHDAQIVHIMEEAGLRISPEQWS 301
Db   240 VVQLLYRASCFNVLKRDGESSLMQLKEEFRTYESLRREHDSQIVQIAFESGLRIGPDQWS 299

Qy   302 SILYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGFDPAN-------LNRLRP 352
Db   300 ALLYADQSHRSHMQSIIDKLQSKNSYQQGVEELRAL---AGSQTSMLVPAYRYFLTQVIP 356

Qy   353 HLELLANIDPNDAVSPTWEQLENAMVAVKTVVHGLVDFIQNY--------SRKGHETPQPQNS 409
Db   357 CLEFFAGIEHEDTSMRMIGDALHQIRILLK--LHCSQDDLRKMPKEBRRGVILQAEVPGG 414

Qy   410 KYKTSMCRDLRQGGCRPGTNCTFPAHSQEELEKYRLRNKKINATVRTEFPLLNKVGVNNTV 469
Db   415 ---------------MGGGGGGSG----------GAEAGRI--- 430

Qy   470 TTTAGNVISVIGSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGA 529
Db   431 ----GGLHPLYSQIDETGRSISRTNPKDNSHNSPQ--- 461

Qy   530 NGQNAAGPSADSVTENKIGSPPRKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVY 589
Db   462 ------------------TPPKQPQRKRYQMGIPPNRMG----- 497

Qy   590 PFHSENIQYFQDRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNVPESSLPP 649
Db   498 PPP----QFFNS--QHLPQRFRGRQRGAPPPPPQP------MPMLIGYD------MPG 539
```

```
Qy   650 ASMPYADHYSTFSPRDRMNSSP-------YQPPPQPYGPVPVPVPSGMYAPVDYDSRRIWRPP 704
Db   540 APMMQATEVLT-ADGQMVNGTPQRVVIMQSPTHLPGGPVVMIPQQQMVPPPQSMTPVGGP 598

Qy   705 MYQRDDIIRSNLPPMDVMHSSV-YQTSLRERYNSLDGYYSV---ACQPPSERRTTV 757
Db   599 M---------------------GPMGMTPSIPVQVPPNTMWTATSPTGSVIVPAASPPGQPHTI 643


RESULT 8
US-10-104-047-3665
; Sequence 3665, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
;   APPLICANT: HELIX RESEARCH INSTITUTE
;   TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
;   FILE REFERENCE: H1-A0105
;   CURRENT APPLICATION NUMBER: US20030236392A1e1 full length cDNA
;   CURRENT FILING DATE: 2002-03-25
;   PRIOR APPLICATION NUMBER:
;   PRIOR FILING DATE:
;   NUMBER OF SEQ ID NOS: 4096
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 3665
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-104-047-3665

Query Match             9.8%;  Score 611;  DB 4;  Length 522;
Best Local Similarity   34.1%;  Pred. No. 2.3e-33;
Matches  187;  Conservative  76;  Mismatches 187;  Indels  98;  Gaps  27;

Qy   618 YYPPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPP 677
Db     2 YYTPPP--------QCVSRFVR----PPPSAPEPAPPYLDHYPPYL-QERVVNSQYGTQPQ 49

Qy   678 QPYGPVPVPVPSGMYAPVDSRRIWRPPMYQRDDIIRSNLPPMDVMHSSV--YQTSLRER 735
Db    50 Q------YPPI----YPSHYDGRRVVPAPSYTREEIFRESPI-PIEIPPAAVPSYPESRER 100

Qy   736 YNSLDGYYSVACQP-------PS---EPRTTVPLPREPCGHLKTSCEEQIRRKPDQWAQYHT 787
Db   101 YQQIESYYPVAPHPTQIRSYLREPPYSRLPPPPQP---HPSLDELHRRRKEIMAQLEE 156

Qy   788 QKAPLVSSTLPVATQSPTTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSC 847
Db   157 RK---VISPPFFA-PSPTLP-PTFHPEEFLDEDLKVAG-KYKGNDYSQYSPWSCDTIGSY 210

Qy   848 INAIDSEPKDVIANSNAVLMDLDGDVKRRVHLFETQRRTKE--EDPIIPFSDGPIISKW 905
Db   211 IGTKDAKPKDVVAAGSVEMMNVESKGM--RDQRLDLQRRAAETSDDLLIPFGDRPTVSRF 268

Qy   906 GAIRSRSSRTGYHTTDPVQATASQGSAATKPISVSDYVPYVNAVDSRW--SSYG--NEATSS 961
Db   269 GAISRTSKIIYQGAGPMQAMAPQGAPTKSINISDYSPY---GTHGGWGASPYSPHQNIPSQ 326

Qy   962 AHYVERDRFIVTDLSGHRK--HSSTGDLLSLELQQ--------------AKSNSLLQR 1004
Db   327 GHFSERERLSMSEVASHGKPLPSAEREQLRELELQQLNHQISQQTQLRGPEAVSNRLVLQR 386

Qy  1005 EANALAMQQ------------KWNSLDEGRHLTLNL--LSKEIELRNGELQSDYTEDATDTKPD 1054
Db   387 EANTLAGQSQPPPPPPKWPGMISSEQLSLELHQVERETGKRTRELSME-NQCSLDMK-- 443

Qy  1055 RDIELELSALDTDE--PDGQSEPIEEILDIQLGISSQNDQLLNGMAVENGHPVQQHQKEP 1112
Db   444 ------SKLNTSKQAENGQPEPQNKV----------PAEDLTLTFSDVPNGSALTQENISL 488

Qy  1113 PKQKKQSL 1120
Db   489 LSNKTSSL 496
```

```
RESULT 9
US-11-072-512-3665
Sequence 3665, Application US/11072512
Publication No. US20060299945A1
GENERAL INFORMATION:
  APPLICANT: ISOGAI, TAKAO
  APPLICANT: SUGIYAMA, TOMOYASU
  APPLICANT: OTSUKI, TETSUJI
  APPLICANT: WAKAMATSU, AI
  APPLICANT: SATO, HIROYUKI
  APPLICANT: ISHII, SHIZUKO
  APPLICANT: YAMAMOTO, JUN-ICHI
  APPLICANT: ISONO, YUUKO
  APPLICANT: HIO, YURI
  APPLICANT: OTSUKA, KAORU
  APPLICANT: NAGAI, KEIICHI
  APPLICANT: IRIE, RYOTARO
  APPLICANT: TAMECHIKA, ICHIRO
  APPLICANT: SEKI, NAOHIKO
  APPLICANT: YOSHIKAWA, TSUTOMU
  APPLICANT: OTSUKA, MOTOYUKI
  APPLICANT: NAGAHARI, KENJI
  APPLICANT: MASUHO, YASUHIKO
  TITLE OF INVENTION: Novel full length cDNA
  FILE REFERENCE: 084335-0191
  CURRENT APPLICATION NUMBER: US/11/072,512
  CURRENT FILING DATE: 2005-03-07
  PRIOR APPLICATION NUMBER: US 60/350,978
  PRIOR FILING DATE: 2002-01-25
  PRIOR APPLICATION NUMBER: 2001-11-05
  PRIOR FILING DATE: 2001-11-05
  PRIOR APPLICATION NUMBER: JP 2001-379298
  NUMBER OF SEQ ID NOS: 4096
  SEQ ID NO 3665
  SOFTWARE: Patentin Ver. 2.1
  LENGTH: 522
  TYPE: PRT
  ORGANISM: Homo sapiens

Query Match             9.8%;  Score 611;  DB 6;  Length 522;
Best Local Similarity   34.1%;  Pred. No. 2.3e-33;
Matches  187;  Conservative  76;  Mismatches  187;  Indels  98;  Gaps  27;

Qy   618 YYPPPPTVPAGVAPCYPRFFVRSNNVPESSLLPPASMPYADHYSTFSFSPRDRMNSSPYQPPPP 677
             ||| ||          |  :|        || :|  ||||||  |  :: |     | |: ||
Db     2 YYTPPP----------QCVSRFVR----PPPSAPEPAPVLDHYPPYL-QERVVNSQYGTQPQ 49

Qy   678 QPYGPVPPVPSGMYAPVYDSRRIWRPMYQRDDIIRSNSLPPMDVMHSSV--YQTSLRER 735
         |   |  :      |  | ||||  |  |:::  :  || :: ::  ||  : :|:||
Db    50 Q----YPPI---YPSHYDGRRVPAPSYTREEIFRESPI-PIEIPPAAVPSYVPESRER 100

Qy   736 YNSLDGYSYSVACQP-----PS---EPRTTVPLPREPCGHLKTSCEEQIRRKPDQWAQYHT 787
         | :: || |  :: :     |:   |||:|  | |   | |   :|:|| |:| | : |
Db   101 YQOIESYYPVAPHPTQIRPSYLREPYSRLPPPQP---HPSLDELHRRKRKBIMAQLEE 156

Qy   788 QKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSSC 847
         :|   ||   | ||:| |  | :| || ||| ||  ||| ||  | |||||||| |||| |
Db   157 RK---VISPPPPA-PSPTLP-PTFHPEEFLDEDLKVAG-KYKGNDYSQYSPWSCDTIGSY 210

Qy   848 INAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKE--EDPIIPFSDGPIISKW 905
         | : | |||| | :: ::  |  ||| ||:   |  :| ||  ||:||||:|| | ||
Db   211 IGTKDAKPKDVVAAGSVEMMNVESKGM--RDQRLDLQRRAAETSDDDLIPFGDRPTVSRF 268

Qy   906 GAISRSSRTGYHTTDPVQOATASQGSATKPISVSDYVPYVNAVDSRW--SSYG--NEATSS 961
         |||||| :   :    : |: : ||| ||||::||| ||   | |:|  |::|  ||: |
Db   269 GAISRSKTIYQGAGPMQAMAPQGAPTKSINISDYSPY--GTHGGWGASPYSPHQNIPSQ 326

Qy   962 AHYVERDRFIVTDLSGHRK--HSSTGDLLSLELQQ------------AKSNSLLLQR 1004
         ||  ||:|: : | :: :|  | | ||| ||||||            ||||| || |:
Db   327 GHPSERERISMSEVASHGKPLPSAEREQLRLELQQLLHQISQQTQLRGPEAVSNRLVLQR 386

Qy  1005 EANALAMQQ------------KWNSLDEGRHLTLNL--LSKIELRNGELQQSDYTEDATDTKPD 1054
         ||  || ||            ||    |  : ::    :|:||  |: |:|| ||      ::
Db   387 EANTLAGQSQPPPPPPPKWPGMISSEQLSLELHQVEREIGKRTRELSME-NQCSLDMK-- 443

Qy  1055 RDIELELGSALDTDR--PDGQSEPIEEHLDIQLGISSQNDQLLNGMAVENGHPVQQHQKEP 1112
         |:|:|   | :|::   | |||| || | ||:         |  :|||:  |:  | |::
Db   444 ------SKLNTSKQAENGQPEPQNKV-------PAEDLTLTFSDVPNGSALTQENISL 488

Qy  1113 PKQKKQSL 1120
         | |||:|
Db   489 LSNKTSSL 496

RESULT 10
US-09-867-550-1346
Sequence 1346, Application US/09867550
Patent No. US20020082206A1
GENERAL INFORMATION:
  APPLICANT: Leach, Martin D.
  APPLICANT: Mehraban, Fuad,
  APPLICANT: Conley, Pamela
  APPLICANT: Law, Debbie
  APPLICANT: Topper, James
  TITLE OF INVENTION: No. US20020082206A1e1 Polynucleotides from Atherogenic Cells and ...
  FILE REFERENCE: 21402-013 (Cura-313)
  CURRENT APPLICATION NUMBER: US/09/867,550
  CURRENT FILING DATE: 2001-05-30
  PRIOR APPLICATION NUMBER: USSN 60/208,427
  PRIOR FILING DATE: 2000-05-30
  NUMBER OF SEQ ID NOS: 2125
  SOFTWARE: FastSEQ for Windows Version 4.0
  SEQ ID NO 1346
  LENGTH: 95
  TYPE: PRT
  ORGANISM: Homo sapiens
US-09-867-550-1346

Query Match             7.9%;  Score 490;  DB 3;  Length 95;
Best Local Similarity   100.0%;  Pred. No. 4.1e-26;
Matches  95;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  1097 MAVENGHPVQQHQKEPPKQKKQSLGEDHVILEQKTILPVTSCFSQPLPVSISNASCLPI 1156
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MAVENGHPVQQHQKEPPKQKKQSLGEDHVILEQKTILPVTSCFSQPLPVSISNASCLPI 60

Qy  1157 TTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS 1191
         |||||||||||||||||||||||||||||||||||
Db    61 TTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS 95

RESULT 11
US-09-864-761-48290
Sequence 48290, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
  APPLICANT: Penn, Sharron G.
  APPLICANT: Rank, David R.
  APPLICANT: Hanzel, David K.
  APPLICANT: Chen, Wensheng
  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
  FILE REFERENCE: Aeomica-X-1
  CURRENT APPLICATION NUMBER: US/09/864,761
  CURRENT FILING DATE: 2001-05-23
  PRIOR APPLICATION NUMBER: US 60/180,312
  PRIOR FILING DATE: 2000-02-04
  PRIOR APPLICATION NUMBER: US 60/207,456
  PRIOR FILING DATE: 2000-05-26
  PRIOR APPLICATION NUMBER: US 09/632,366
  PRIOR FILING DATE: 2000-08-03
  PRIOR APPLICATION NUMBER: GB 24263.6
  PRIOR FILING DATE: 2000-10-04
```

; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

; NUMBER OF SEQ ID NOS: 49917
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 48290
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: MAP TO AL136170.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: SWISSPROT HIT: Q01970, EVALUE 2.60e+00
; OTHER INFORMATION: EST_HUMAN HIT: AW962574.1, EVALUE 4.00e-32
US-09-864-761-48290

Query Match   5.0%;   Score 311;   DB 3;   Length 67;
Best Local Similarity 89.6%;   Pred. No. 6.4e-14;
Matches 60; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 254 VTKRDEDDSLMQLKEEFRSYEALRREIDAQIVHIAMEAGLRISPEQWSSLLYGDLAHKSH 313
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 VTKRDEDDSLMQLKEEFRTYEALRREHDSQIVQIAMEAGLRIAPDQWSSLLYGDQSHKSH 60

RESULT 12
US-10-450-763-41493
; Sequence 41493, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 41493

Db 314 MQSIIDK 320
            |||||||
Qy   61 MQSIIDK 67

; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (63)..(105)
; OTHER INFORMATION: Riboasomal protein L30e proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00709B, p-value=5.313e-28, raw score of 21.58
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (171)..(201)
; OTHER INFORMATION: Zinc finger, C3HC4 type (RING finger) domain identified by
; OTHER INFORMATION: PFam, accession name zf-C3HC4, E-value=0.014, PFam score of 12.6
US-10-450-763-41493

Query Match   4.3%;   Score 267;   DB 5;   Length 276;
Best Local Similarity 59.8%;   Pred. No. 6.5e-10;
Matches 52; Conservative 9; Mismatches 10; Indels 16; Gaps 2;

Qy   8 WTEFLSCPICYNEEFDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTDIDVLPVN 67
            |||||||||||||||||||||||||||||||||||||||||||||||||||::|||||
Db 168 WT--------------FDETIRKPISLGCGHTVCKMCLNKLHRKACPFDQTTINTDIELLPVN 216

Qy   68 FALLQLVGAQVPFDHQSIKLSNLGENKH 94
            |||||||||| |||||
Db 217 SALLQLVGA-----QALKITKILTDLH 238

RESULT 13
US-10-330-773-941
; Sequence 941, Application US/10330773
; Publication No. US20060042262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 52945Z001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 941
; LENGTH: 1552
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-330-773-941

Query Match   3.3%;   Score 208;   DB 5;   Length 1552;
Best Local Similarity 22.0%;   Pred. No. 0.00012;
Matches 148; Conservative 82; Mismatches 190; Indels 252; Gaps 36;

Qy 572 LNSVPQKSSPFLTRVPVYPPH--------SENIQYFQDPRTQIPFEVPQYPQ--------TGYYPP 621
            ||||| || | |: |:|| |||
Db   1 MNSQPQTRSPFFQRPQIQPPRATIPNSSPSIR------PGAQTPTAVYQANQHIMVNHLPM 56

Qy 622 PPTVPAGVAPCVPRRVRSNNVPESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPQPYG 681
            |||||:||:||: |::||||| ||:
Db   57 PYPVPQGPQYCIPQYRHSG-----------------PPYVGPPQQY------PVQPGPGPFY 96

Qy 682 PVP--PVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSSVYQTSLRERYNS 738
            ||:   ::| ||:| |:|
Db   97 PGPGPGCDFPNAYGTPFYPSQ-----PVYQSAPII----VPTQQ---------- 130

Qy 739 LDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIR-RKPDQWAQYHTQKAPLVSS-- 795
            | ||:: |::| |:|
Db 131 -----------QPP------------PAKRE-----------KKTIRIRDPNQGGKDITEE--IMSGGG 163

Qy 796 ------TLPVA-TQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSCIN 849
            ||| |:: |::|||||: |
Db 164 SRNPPPIGRPTSTPTPPQQLPSQ--VPEHSPVVGT-VESAHLAASTPVTA----- 212

Qy 850 AIDS-------EPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGPIIS 903
            ||| |:||| | :|::| ::|| || |: |:|:
Db 213

RESULT 14

US-10-840-512-196

Sequence 196, Application US/10840512
Publication No. US20050125852A1

GENERAL INFORMATION:

```
 APPLICANT:  CAENEPEEL, SEAN
 APPLICANT:  MANNING, GERARD
 APPLICANT:  CHARYDCZAK, GLEN
 APPLICANT:  GRIGORIEV, IGOR
 TITLE OF INVENTION: NOVEL KINASES
 FILE REFERENCE: 034536-1455
 CURRENT APPLICATION NUMBER: US/10/840,512
 CURRENT FILING DATE: 2004-05-07
 PRIOR APPLICATION NUMBER: 60/469,014
 PRIOR FILING DATE: 2003-05-09
 NUMBER OF SEQ ID NOS: 239
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 196
 LENGTH: 2377
 TYPE: PRT
 ORGANISM: Mus musculus
```

US-10-840-512-196

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  Query Match    3.3%;  Score 207;  DB 5;  Length 2377;
  Best Local Similarity  19.3%;  Pred. No. 0.00027;
  Matches 216;  Conservative 152;  Mismatches 424;  Indels 326;  Gaps 46;
```

```
Qy     48 KACPFDQTAINT---------------------------DIDVLPVNFALLQLVGAQVPDHQSIKLSNLGEN 92
                                                    |:|| |  | | |: :| | |:: :|  | |:
Db    375 KRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLEMATSEYP------------------------ 421

Qy     93 KHYEVAKKCVEDLALYLYLKPLSGGKGVASLNQSAL----------------SRPMQRKLVTLVN 139
           : ::  |  |  |  : | :|:| | | | |    | |               | :|| :| : :
Db    422 -----YSECQNAAQIYRVTSGVK--PASFDKVAIPEVKEIIEGCIRQNKDERYSIKDLIN 475

Qy    140 COLVEEGRVRAMRAARSLGERTVTELLLQHQNPQQLSANLWAAVRARGCOFIGPAMOEE 199
              | : | | : | | :|  :  | |  | :   | ||  | | | :||    | |:
Db    476 HAFFQEETGVRVELAEDDGEKIAIKLWLRIEDIKKLK------------------GKYKDNE 520

Qy    200 ALKLVLILALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQ------------LLYRAS 250
           || :| :|  | |  | |    |     | :          :  |            ||  |
Db    521 AIEF-----------SFDLERVDPEDVAQEMVESGYVCEGDHKTMAKAIKDRVS 563

Qy    251 CFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGIRISPEQWSSLLYGDLAH 310
                 |::  |  | :  |::         |   : : |  | | :  | | | |  ||
Db    564 LIK-RKPBQRQLVREEQERKQEBSSFKQONEQQASVS--QAGI----QQLSAASTGIPTA 617
```

```
; ORGANISM: Arabidopsis thaliana
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(674)
;   OTHER INFORMATION: Ceres Seq. ID no. 1828460
US-11-096-568A-27756

Query Match             3.3%;  Score 203;  DB 6;  Length 674;
Best Local Similarity   23.1%;  Pred. No. 7.2e-05;
Matches 137;  Conservative 58;  Mismatches 209;  Indels 190;  Gaps 30;

Qy      353 HLELLANID----------------------PNPDAVSPTWEQLE------NAMVAVKTVVHGLVDFIQNYS 396
                |::|:|||::                                               ||:
Db       35 HMKLLFELDLSNNRFVGKFPNVVLSLPSLKFLDLRYNEFEGGSIPSKLFDKELDAIFLHHN 94

Qy      397 RKGHETPQPQPNSKYKTSMCRDLRQQGGCPRGTNCTFAHSQEELEKYRLRNKKINA---- 452
                ::|                 |::                                      :
Db       95 RPMFGIPENMGNSPVSALVLAD-NDLGGCIPG---SIGLMGKTLNEILLSNDNLTGCLPP 150

Qy      453 -----TVRTFPL-LNKVGVNNTVTTAGNVISV--------IGSTETTGKIVPSTNGISNAEN 501
                 |::|||: |: |:| |:            ||: |   ||:        ||||||||
Db      151 QIGNLKNVTVFDISFNR--LSGPLPSSIGNMKSLEQLNVANNRFTGVIPSSICQLSNLEN 208

Qy      502 SVSQLISRSTDSTLRALETVKCKVG--KVGANG------------QNAAGPSADSVTENK 546
                                  ::::                                :::
Db      209 ---PTYSSNFFTGDAPRCVALLGDNVVVNGSMNCIDGKEDQRSSKECSSPASRSVDCSK 264

Qy      547 IGS--------------------------PPKTPVSNVA--------------ATSAGPSN 567
                                             ||:|:                    :|:
Db      265 FGCNNFFSPPPPSFKMSPTVRVLPPPPPSSKMSPTFRATPPPPSSKMSPSFRATPPPPSS 324

Qy      568 -VGTELNSVP-----QKSSPFLTRVPVYPPHSENIQYFQDPRTQIPFEVPQYPQTGYYPP 622
                 :||                  ||:|  |:|||               |||
Db      325 KMSPSFRATPPPPSSKMSPSVKAYPPPPPPEYEPSPPPPPSSEMSPSVRAYP----PPP 379

Qy      623 PTVPAGVAPCVPRFVRSNNVPESSLPP----------------ASMPYADHYSTFSPR 664
                |:   |   |                                   ::|     ||||
Db      380 PLSPPPSP-PPPYIYSSPPPPSPSPPPYIYSSPPPVVNCPPTTQSPPPKYEQTPSPR 438

Qy      665 D--RMNSSPY------QPPPPQPY---GPVPPVPSGMYA----------PVYDSRRIWRPPMY 706
                    ||  ||       |::|||     ||| ||| ||:           |:
Db      439 EYYPSPSPPYYQYTSSPPPTYYATQSPPPPPPTYYAVQSPPPPPPYYV-----YPPV- 491

Qy      707 QRDDIIRSNSLPPMDVMHSSVYQTSLRERYNSLDGYYSVACQ---PPSPRTTVPLPRBPC 764
                |:   |||  | || |     ||               ::          :|
Db      492 -------TASPPPPVVYTPVIQSPPPPV----YSPVTQSPPPPPVYYPPPVTQSP- 538

Qy      765 GHLKTSCEEQIRRKPDQWAQYHTQKAPLVSST------LPVATQSPTPPSPLF 811
                                                      |||||||:|||:|:
Db      539 --------------PPSPVYY---PPVTQSPPPPPVYYLPV-TQSPPPPSPVY 573
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Search completed: May 24, 2006, 12:53:32
Job time : 116 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM protein - protein search, using sw model

                    GenCore version 5.1.8
                    Copyright (c) 1993 - 2006  Bioacceleration Ltd.

Run on:             May 24, 2006, 12:51:45 ; Search time 10 Seconds
                                            (without alignments)
                                            1326.457 Million cell updates/sec

Title:              US-10-619-992-2
Perfect score:      6215
Sequence:           1 MPVQAAQWTEFLSCPICVNE..........MSEDKNDFLKPVANGKMVNS 1191

Scoring table:      BLOSUM62
Searched:           Gapop 10.0 , Gapext 0.5
                    56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters:        56051

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published Applications AA New:*
            1:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
            2:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
            3:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
            4:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
            5:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
            6:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
            7:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
            8:   /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	177	2.8	1812	6	US-10-480-434A-14	Sequence 14, Appl
2	171	2.8	577	7	US-11-293-697-3929	Sequence 3929, Ap
3	166.5	2.7	3429	6	US-10-953-349-1430	Sequence 1430, Ap
4	166.5	2.7	3438	6	US-10-953-349-9275	Sequence 9275, Ap
5	166.5	2.7	3478	6	US-10-953-349-9273	Sequence 9273, Ap
6	159.5	2.6	1809	6	US-10-559-415-190	Sequence 190, Appl
7	159.5	2.6	1919	6	US-10-559-415-2	Sequence 2, Appli
8	159	2.6	1057	7	US-11-293-697-3230	Sequence 3230, Ap
9	159	2.6	443	6	US-10-953-349-13469	Sequence 13469, A
10	158.5	2.6	451	6	US-10-953-349-13468	Sequence 13468, A
11	158.5	2.6	456	6	US-10-953-349-13467	Sequence 13467, A
12	158	2.5	240	6	US-10-953-349-16346	Sequence 16346, A
13	153	2.5	1384	6	US-10-505-928-799	Sequence 799, App
14	152	2.4	950	7	US-11-293-697-4492	Sequence 4492, Ap
15	151	2.4	343	6	US-10-953-349-21437	Sequence 21437, A
16	148.5	2.4	837	6	US-10-953-349-9736	Sequence 9736, Ap
17	148.5	2.4	846	6	US-10-953-349-9735	Sequence 9735, Ap
18	147.5	2.4	692	6	US-10-953-349-9737	Sequence 9737, Ap
19	145.5	2.3	559	6	US-10-953-349-13784	Sequence 13784, A
20	145.5	2.3	575	6	US-10-953-349-13783	Sequence 13783, A
21	145.5	2.3	598	6	US-10-953-349-13782	Sequence 13782, A
22	144.5	2.3	448	6	US-10-953-349-8748	Sequence 8748, Ap
23	142	2.3	634	7	US-11-293-697-3340	Sequence 3340, Ap
24	140.5	2.3	694	6	US-10-505-928-312	Sequence 312, App
25	140	2.3	295	6	US-10-953-349-23677	Sequence 23677, A
26	140	2.3	849	6	US-10-953-349-1432	Sequence 1432, Ap
27	140	2.3	1003	6	US-10-953-349-1431	Sequence 1431, Ap
28	140	2.3	1392	6	US-10-953-349-1430	Sequence 1430, Ap
29	139.5	2.2	296	6	US-10-953-349-8749	Sequence 8749, Ap
30	139.5	2.2	693	7	US-11-293-697-3849	Sequence 3849, Ap
31	139	2.2	652	6	US-10-953-349-5551	Sequence 5551, Ap
32	138.5	2.2	227	6	US-10-953-349-20011	Sequence 20011, A
33	137.5	2.2	592	6	US-10-953-349-39541	Sequence 39541, A
34	137.5	2.2	592	6	US-10-953-349-39540	Sequence 39540, A
35	137.5	2.2	610	6	US-10-953-349-39539	Sequence 39539, A
36	137	2.2	564	6	US-10-511-937-2557	Sequence 2557, Ap
37	136	2.2	155	6	US-10-953-349-15526	Sequence 15526, A
38	136	2.2	173	6	US-10-953-349-15525	Sequence 15525, A
39	136	2.2	812	7	US-11-293-697-3673	Sequence 3673, Ap
40	136	2.2	4373	6	US-10-511-118-524-2	Sequence 2, Appli
41	135	2.2	293	6	US-10-953-349-31470	Sequence 31470, A
42	134	2.2	681	6	US-10-953-349-10919	Sequence 10919, A
43	133.5	2.1	454	7	US-11-293-697-3595	Sequence 3595, Ap
44	133	2.1	778	7	US-11-293-697-3043	Sequence 3043, Ap
45	132.5	2.1	161	6	US-10-953-349-18169	Sequence 18169, A

ALIGNMENTS

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RESULT 1
US-10-480-434A-14

; Sequence 14, Application US/10480434A
; Publication No. US20060105403A1
; GENERAL INFORMATION:
; APPLICANT: DALLA VENEZIA, NICOLE
; APPLICANT: MAGNARD, CLEMENCE
; APPLICANT: SINILNIKOVA-ERARD, OLGA
; TITLE OF INVENTION: BRCA1/ACC ALPHA MOLECULAR COMPLEXES, DIAGNOSTIC AND
; TITLE OF INVENTION: THERAPEUTIC APPLICATIONS
; FILE REFERENCE: 0512-1194
; CURRENT APPLICATION NUMBER: US/10/480,434A
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/FR02/02016
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: FR 01/07740
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: FR 02/02789
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
; LENGTH: 1812
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-480-434A-14

  Query Match             2.8%;  Score 177;  DB 6;  Length 1812;
  Best Local Similarity   18.2%;  Pred. No. 0.036;
  Matches  232;  Conservative  167;  Mismatches  470;  Indels  406;  Gaps   55;

Qy         10 EFLSCPICVNEFDENVHKPISLGCSHTVCKTCLNKLHRK-----ACPFDGTAINTDIDVL 64
              |  |||||   :|||    : ||  | ||   | :            : :| :  |    |
Db         20 KILECPICL----ELIKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNEIT----- 69

Qy         65 PVNFALLQLVGAQVPDHQSIKLSNILGENKHIYEVAKKCVEDLALYLKPLSGGKGVASLNQS 124
                 :| | | |           :  ||||  |   ::     |   :         :  |
Db         70 ------------------KRSLQGSTRFSQLA----EELLRIMAAFELDTGMQLTNGF 105

Qy        125 ALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNFQQLSANLWAAV 184
              | |:  :|:  |: :| |  | : ||   : | |    |   |:     : |  : |
Db        106 SFSKKRNN-----SCERLNEEASI----IQSVGYRNRVRRLFQVEP----------- 142

Qy        185 RARGCOFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQ 244
                 | : ||     : || | :||  |    | : |  | | :  |       | ||:
Db        143 --------GNATLKDSL--------GVQLSNLGIVRSVKKN---ROTQPRKSV--YIE 180

Qy        245 LIYRASCFKVTKRDE-----DSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLR-ISPEQ 299
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RESULT 2

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Db   181 LDSDSSEETVTKPGDCSVRDQELLQTAPQEAGDEG--KLHSAEEAACEFSEGIRNIEHHQ 238

Qy   300 WSSLLYGDLAIKSHMQSIIDKLQSPSFAKSVQELTIVLQRTGDPANLRLRPHLELLAN 359
Db   239 CSDDLNPTENHATE------RHPEK-CQSISISNVCVEPCCGTDAHASSLQPETSSLLL 289

Qy   360 IDPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSR----KGHETPQPQNSKYKTSM 415
Db   290 IEDRMNA------EKAEFCNKSKQPGIA--VSQQSRWAASKGTCNDRQVPSTGEKV-- 337

Qy   416 CRDLRQQGCGPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTAGN 475
Db   338 ------GPN--ADSLSDREKW------THP--QSLCPENSGATTDVP 368

Qy   476 VISVIGSTE------TTGKIVPSTNGI--SNAENSVSQLISRSTDSTLRALETVKK 523
Db   369 WITLNSSVQKVNEWFSRTGEMLTSDSASARRHESNAEAAVVLEVSNEVDG--GFSSSRK 425

Qy   524 VGKVG------ANGQNAAGPSADSVTENKIGSPPKTPVSNVAATSAGPSNVGTELNS 574
Db   426 TDLVTPDDHHTLMCKSGRDFSKPVEDNISDKIFGKSYQRKGSR-------PHLNH 473

Qy   575 VPQKSSPPLT--RVPVYPPHSENIQYFQDPRTQIPPEVPQYPQTGYYPPPPTVPAG---V 629
Db   474 VTEIIGTFITEPQITQEQPFTNKLKRKRSTSLQPEDFIKADSAGVQRTPDNINQGTDLM 533

Qy   630 APCVPRFVRSNNVPESSLPPASMPYADHYSTFSPRDRMNSSPYQPPPPQYPGEVPPVPSG 689
Db   534 EPNEQAVSTTSNCQENKIAGSNL--QKEKSAHPTESLRKEP 572

Qy   690 MYAPVVDSRRIWRPPMYQRDDIIRSNSLPPMDV--MHSSVYQTSLRERYNSLDGYYSVA 746
Db   573 -ASTAGAKSI--SNSVSDLEVELNVHSSKAPKKNRLRRKS-----SIR 612

Qy   747 CQPPSEPRTTVPLPREPCGHLKT----SCEEQIRRKPDQWAQYHTQKAPLVSSTLPVATQ 802
Db   613 CALPLEPISRNPSP-PTCAELQIDSCCGSSEETKKNHSNQQPAGHLREPQLIEDTEPAADA 671

Qy   803 SPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSSCINAIDSEPKDVIANS 862
Db   672 KKNEPN------EHIRKR------RASDAFPEEKLMNK 697

Qy   863 NAVLMDLLDSGSDVKRRVHLFETQRRTKEEDPIIPFSDGPIISKNGAISRSSRTGYHTTDPV 922
Db   698 AGLLTSCSS------PRKSQGPVNP-------SPQRTGTEQLETR 729

Qy   923 QATAS------QGSATKPISVSDYVPYVNAVDSRWSSSYGNEATSSAHYVERDR 969
Db   730 QMSDSAAKELGDRVLGGGEPBSGKTTDRSESTSVSLVS--DTYDTQNSVSVLDAHTV--- 783

Qy   970 FIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDEG------RHL 1024
Db   784 ------RYARTGSAQCMTQFVASENPKELVHGSN------NAGSGTEGLKPPLRH- 826

Qy  1025 TLNLLSKEIELRNGELQSDYTE------DATDTKPDRDIELELS 1062
Db   827 ALNLSOEKVEMEDSELDTQYLQNTFQVSKRQSPFALFSKPRSPQKDCAHSVPSKELSPKVT 886

Qy  1063 ALDTD--EPDGQSEPIEEILDIQ------LGISSQNDQLLNGMAVENGHPV--QQHQKEP 1112
Db   887 AKGKQKERQQEB--FEISHVQAVAATVGLPVPCQEGKLAADTMCDRGCRLCPSSHYRS- 943

Qy  1113 PKQKKQSLGEDHVILEEQKTILPVTSCFSQPLPVSISNASCLPITTSVSAGNLILKTHVM 1172
Db   944 ------GENG-LSATGKSGISQNSHFKQ------SVSPIRSSI------ 973

Qy  1173 SEDKNDFLKPVANGK 1187
Db   974 --KTDNRKPLTEGR 985
```

RESULT 3

```
Query Match   2.8%; Score 171; DB 7; Length 577;
Best Local Similarity   22.0%; Pred. No. 0.016;
Matches   98; Conservative   50; Mismatches 147; Indels 150; Gaps 20;
```

```
Qy   451 NATVRTFPLLNKVGVNNTVTTAGNVISVIGSTETTGKIVPSTNGISNAENSVSQLISRS 510
Db     4 SASIHSMP------TGTIPPPTIKATGSTHTAPPMTPTTSGTSOQSPSS----FSTA 50

Qy   511 TDSTLRALETVKKVGKVGANGQNAAGPSADSVTENKIGSPPKTPVSNVAATSAGPSNVGT 570
Db    51 KTSTSLPYHT------SSTHHPEVTTPTSTTNIITFKHTSTGTRTPVAH--TTSASSSRLPT 102

Qy   571 EL--NSVPQKSSPPLTRVPV------YPPHSENIQYFQDPRTQIPPEVPQY----- 613
Db   103 PFTTHSPPTGSSPFSSTGPMTATSPQTTTTTYPTPSH------PQTTLPTHVPPFSTSLV 155

Qy   614 ------PQTGYYPPPPTVPA-- 627
Db   156 TPSTHTVIITHTQMATSASIHSTPTGTVPPPTTLKATGSTHTAPPMTTVTTSGTSQTHSS 215

Qy   628 -GVAPCVPRFVRSNN-VPE--SSLPPAS----MPYADHYSTFSPRDRMNSSPYQPPPPQ 678
Db   216 FSTATASSSFISSSSWLPQNSSSRRPPSSSPITTQLPHLSSATTPVSTTNQLSFSFSPSPSA 275

Qy   679 PYGPVPPVPSGMYAPVVDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVVQTSLRERYNS 738
Db   276 PSTVSSSYVPSSHSSPQTSS-----PSVGTSBSFV---SAP----VHSTTLSSGSHSSLST 323

Qy   739 LDGYYSVACQP--PSEP------RTTVPLPREPCGHLKTISCEEQIRRKPDQWAQYHTQKA 790
Db   324 HPTTASVSASPLFPSSPAASTTIRATLP------HTISS 356

Qy   791 PL-VSSTLPVA--TQSPTPPSPLFS 812
Db   357 PFTLSALLPISTVTVSPTPSSHLAS 381
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US-10-953-349-9275

Query Match   2.7%;   Score 166.5;   DB 6;   Length 3429;
Best Local Similarity   19.2%;   Pred. No. 0.33;   Mismatches 439;   Indels 331;   Gaps 53;
Matches 219;   Conservative 151;

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Qy  247  YRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLIYG  306
                                                                     
Db 1190  YLESLLRESKKEEDAPV--LDDDALNDLIARRBSEIDIFESIDKQRKENEMETWNTLVHG 1247

Qy  307  DLAHK-SHMQSIIDKLQSPESF------------------AKSVQELTIVLQRT        341
                                                                     
Db 1248  PGSDSFAHIPSIPSRLVTEDDLKLLYETMKLNDVPMVAKESTVGMKRKDGSMGGLDTHQY 1307

Qy  342  GDPANLNRLRPHLELLANID-------PNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQN  394
                                                                     
Db 1308  GRGKRAREVRSYEEKLTEEEFEKLCQTESPDSPQGKGEGSERSLANDTSNIP-----VEN 1362

Qy  395  YSRKGHETPQP-QPNSKYKTSMCRDLRQQGCPRGTNCTFAHSQEELEKYRLRNKKINAT  453
                                                                     
Db 1363  SS-----DTLLPTSPTQAITVQPMEPVRPQ---------SHTLKEETQPIKRGRGRPK---- 1406

Qy  454  VRTFPLLNKVGVNNTVTTTA-GNVISVIGSTETTGKIVPSTNGISNAENSVSQLISRSTD  512
                                                                     
Db 1407  -RTDKALTPVSLSAVSRTQATGNAIS---SAATGLDFVSSDKRLEAASHPTSSLALTSPD 1462

Qy  513  -----------------STLRALETVKKVGKVGANGQNAAG----PSADSVTENKIGSPPKT  553
                                                                     
Db 1463  LSGPPGFQSLPASPAPTPIRGRGRSRGRGAGRGRRVEGVLHGSNSSITQR---------   1514

Qy  554  PVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVP----------------VYPPHS------  593
                                                                     
Db 1515  ---TETATSLASDAEATKF-ALPRSASEIVSRVPKANEGSTSNPDQVSPVHSATTALRSD  1570

Qy  594  -------ENIQYFQDPRTQIPFEVPQYP---------QTGYYPPPTVP-------        626
                                                                     
Db 1571  KAADKDLDAPPGFDSGSHVQTLNVLENSSERKAFAVKKRPLIQGVSSQHPGPNKQPLDLP 1630

Qy  627  ------AGVAPCVPRFVRSNNVPESSLPPASMPY-ADHYSTFSPRDR---MNSSPYQ--    673
                                                                     
Db 1631  VSTSSTLLGGGPVQNQNAVSSVCDGSKSPSEGRTYTALQGVTTAPSDATLPMSSQPSDAT 1690

Qy  674  ---PPPPQPYGP---------YYSVACQPPSEPRTTVPLPREPCHLKTSCE           721
                                                                     
Db 1691  LPMSSQPVGSTVEAQEANVPSLPAALPA-----KRVRNLPSRGETPKRQGKRRGQPLPAT 1746

Qy  721  DVMHSSYYQTSL-----------RERYNNSLDG-------PDIHSSGSLS            772
                                                                     
Db 1747  DA--SSARSTGLTPQIEVKVGNLSGTKAKFDAVAKEQPHFSQSVA------           1799

Qy  773  EQIRR------------------KPDQWAQYHTQKAPLVSSTLPVATQSPTPSP-       809
                                                                     
Db 1800  QEIRRDITSGTGGSARKQTADVTDVARVWMKEIFSETSLLKHKVGEPSATTRTNVPDAQSPG 1859

Qy  810  ---------LFSVDFRADFSESVSGTKFEE----------DHLSHYSPWSCGTIGSCINAIDSE 854
                                                                     
Db 1860  EMNLHTVETHK--ABDSSGLKNQEALYNLSKADKLVSDIPHPVPGDLTTSGSVAN----   1912

Qy  855  PKDVIANSNAV--------LMDLDSGDVKRRV---HLFET------QRRTKEE         890
                                                                     
Db 1913  -KDVDIGSSKVAAENELVKIPGGDVDSSVIQLSLGNTLTAKSSLEKCTADQLLGEKLSQE 1971

Qy  891  DPIIPFSDGPIISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPVNAVDSR  950
                                                                     
Db 1972  GETTPASDGETCHL--AEBETASSLSYRSEP--TASASTTAEPLPTDKLEKNISFQDE-  2025

Qy  951  WSSYGNEATSSAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSILLQREANALA 1010
                                                                     
Db 2026  --------------------VKTLNGDKREAI---LLSSE-EQTNVNSKI---ETNSEE  2057

Qy 1011  MQQKWNSLDEGRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPD 1070
                                                                     
Db 2058  LQA---SRTDEVPHVD-------GKSVDVANQTVKED------EAKHSVEIQSSMLEPDELP 2103
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RESULT 4
US-10-953-349-9274
; Sequence 9274, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;   APPLICANT: ALEXANDROV, Nickolai et al.
;   TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;   TITLE OF INVENTION: ENCODED THERBY
;   FILE REFERENCE: 2750-1579PUS2
;   CURRENT APPLICATION NUMBER: US/10/953,349
;   CURRENT FILING DATE: 2004-09-30
;   NUMBER OF SEQ ID NOS: 40252
;   SOFTWARE: Patentin version 3.3
; SEQ ID NO 9274
;   LENGTH: 3438
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-953-349-9274

Query Match   2.7%;   Score 166.5;   DB 6;   Length 3438;
Best Local Similarity   19.2%;   Pred. No. 0.33;   Mismatches 439;   Indels 331;   Gaps 53;
Matches 219;   Conservative 151;

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Qy  247  YRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLIYG  306
                                                                     
Db 1199  YLESLLRESKKEEDAPV--LDDDALNDLIARRBSEIDIFESIDKQRKENEMETWNTLVHG 1256

Qy  307  DLAHK-SHMQSIIDKLQSPESF------------------AKSVQELTIVLQRT        341
                                                                     
Db 1257  PGSDSFAHIPSIPSRLVTEDDLKLLYETMKLNDVPMVAKESTVGMKRKDGSMGGLDTHQY 1316

Qy  342  GDPANLNRLRPHLELLANID-------PNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQN  394
                                                                     
Db 1317  GRGKRAREVRSYEEKLTEEEFEKLCQTESPDSPQGKGEGSERSLANDTSNIP-----VEN 1371

Qy  395  YSRKGHETPQP-QPNSKYKTSMCRDLRQQGCPRGTNCTFAHSQEELEKYRLRNKKINAT  453
                                                                     
Db 1372  SS-----DTLLPTSPTQAITVQPMEPVRPQ---------SHTLKEETQPIKRGRGRPK---- 1415

Qy  454  VRTFPLLNKVGVNNTVTTTA-GNVISVIGSTETTGKIVPSTNGISNAENSVSQLISRSTD  512
                                                                     
Db 1416  -RTDKALTPVSLSAVSRTQATGNAIS---SAATGLDFVSSDKRLEAASHPTSSLALTSPD 1471

Qy  513  -----------------STLRALETVKKVGKVGANGQNAAG----PSADSVTENKIGSPPKT  553
                                                                     
Db 1472  LSGPPGFQSLPASPAPTPIRGRGRSRGRGAGRGRRVEGVLHGSNSSITQR---------   1523

Qy  554  PVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVP----------------VYPPHS------  593
                                                                     
Db 1524  ---TETATSLASDAEATKF-ALPRSASEIVSRVPKANEGSTSNPDQVSPVHSATTALRSD  1579

Qy  594  -------ENIQYFQDPRTQIPFEVPQYP---------QTGYYPPPTVP-------        626
                                                                     
Db 1580  KAADKDLDAPPGFDSGSHVQTLNVLENSSERKAFAVKKRPLIQGVSSQHPGPNKQPLDLP 1639

Qy  627  ------AGVAPCVPRFVRSNNVPESSLPPASMPY-ADHYSTFSPRDR---MNSSPYQ--    673
                                                                     
Db 1640  VSTSSTLLGGGPVQNQNAVSSVCDGSKSPSEGRTYTALQGVTTAPSDATLPMSSQPSDAT 1699

Qy  674  ---PPPPQPYGP---------VPPVPSGMYAPVYDSRRIWRPPMY----QRDDIIRSNSLPPM 720
                                                                     
Db 1700  LPMSSQPVGSTVEAQEANVPSLPAALPA-----KRVRNLPSRGETPKRQGKRRGQPLPAT 1755

Qy 1071  GQSEPIEEILDIQ-LGISSQNDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEE 1129
                                                                     
Db 2104  NAGQKGHSSIDLQPLVLVTSNE------NAMSLDD-------KDYDPISKSADIEQD---- 2147

Qy 1130  QKTILPVTSCFSQPLPVSISNASCLPITTSVSAGN---LILKTHVMSEDKNDFLKPVANG 1186
                                                                     
Db 2148  -----PEBSVFVQ---GVGRPKVGTADTQMEDTNDAKLLVGCSVESEEKEKTLQSSLIPG 2198
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RESULT 5
US-10-953-349-9273
; Sequence 9273, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
;  APPLICANT: ALEXANDROV, Nickolai et al.
;  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;  FILE REFERENCE: 2750-1579PUS2
;  CURRENT APPLICATION NUMBER: US/10/953,349
;  CURRENT FILING DATE: 2004-09-30
;  NUMBER OF SEQ ID NOS: 40252
;  SOFTWARE: Patentin version 3.3
; SEQ ID NO 9273
;  LENGTH: 3478
;  TYPE: PRT
;  ORGANISM: Arabidopsis thaliana
US-10-953-349-9273

  Query Match             2.7%;  Score 166.5;  DB 6;  Length 3478;
  Best Local Similarity   19.2%;  Pred. No. 0.34;
  Matches  219;  Conservative  151;  Mismatches  439;  Indels  331;  Gaps  53;

Qy    721 DVMHSSVYQTSL-----RERYNSLDG------YYSVACQPPSERTTVPLPREPCGHLKTSCE  772
              ::  :     ::  |      :::|::| |
Db   1756 DA--SSARSTGLTPQIEVKVGNLSGTKAKFDAVAKEQPHFSQSVA-----PDIHSSGSLS 1808

Qy    773 EQIRR------                          KPDQWAQYHTQKAPLVSSTLPVATQSPTPPSP-  809
          :|||
Db   1809 QEIRRDTSGTGGSSARKQTADVTDVARVMKEIFSETSLLKHKVGEPSATTRTNVPDAQSPG 1868

Qy    810 ---LFSVDFRADFSESVSGTKFEE-----       DHLSHYSPWSCGTIGSCINAIDSE  854
Db   1869 EMNLHTVETHK--AEDSSGLKNQEALYNLSKADKLVSDIPHPVPGDLITTSGSVAN----  1921

Qy    855 PKDVIANSNAV-----LMDLDSGDVKRRV---HLFET------QRRTKEE  890
              |||              :|  :                 :|
Db   1922 -KDVDIGSSKVAAENELVKIPGGDVDSSVIQLSLGNTLTAKSSLEKCTADQLLGEKLSQE 1980

Qy    891 DPIIPFSDGPIISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSR  950
          ::|                                 :  :
Db   1981 GETTPASDGETCHL--ABETASSLSYRSEP---TASASTTAEPLPTDKLEKNISFQDE- 2034

Qy    951 WSSYGNEATSSAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALA 1010
Db   2035 ------------VKTLNGDKREAI---LISSE-EQTNVNSKI---ETNSEE 2066

Qy   1011 MQQKWNSLDEGRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPD 1070
          |||                        :::
Db   2067 LQA--SRTDEVPHVD-----GKSVDVANQTVKED-----EAKHSVEIQSSMLEPDELP 2112

Qy   1071 GQSEPIEEILDIQ-LGISSQNDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEE 1129
          |:| |||||||||  |:||
Db   2113 NAGQKGHSSIDLQPLVLVTSNE---NAMSLDD-------KDVDPISKSADIEQD 2156

Qy   1130 QKTILPVTSCFSQPLPVSISNASCLPITTSVSAGN---LILKTHVMSEDKNDFLKPVANG 1186
Db   2157 ------PEESVFVQ-----GVGRPKVGTADTQMEDTNDAKLLVGCSVESEEKEKTLQSLIPG 2207

Qy    247 YRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIMEAGIRISPEQWSSLIYG  306
          |: :  |   |:||:|: ||:|||||:  ::|||
Db   1239 YLESLLRESKKEEDAPV--LDDDALNDLIARRESEIDIFESIDKQRKENEMETWNTLVHG 1296

Qy    307 DLAHK-SHMQSIIDKLQSPESF------------AKSVQELIIVLQRT-----  341
          :| :|  |::|:||: |||:|
Db   1297 PGSDSFAHIPSIPSRLVTEDDLKLLYEFMKLNDVPMVAKESTVGMKRKDGSMCGLDTHQY 1356

Qy    342 GDPANLNRLRPHLELLANID------PNPDAVSPTWEQLENAMVAVAXTVVHGLVDFIQN  394
Db   1357 GRGKRAREVRSVERKLTEEEFEKLCQTESPDSPQGKGEGSERSLANDTSNIP-----VEN 1411

Qy    395 YSRKGHETPQP-QPNSKYKTSMCRDLRQQGCRPGTNCTFAHSQEELEKYRLRNKKINAT  453
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Db   1412 SS-----DTLLPTSPTQAITVQPMEPVRPQ----------SHTLKEETQPIKRGRGRRPK- 1455

Qy    454 VRTFPLLNKVGVNNTVTTTA-GNVISVIGSTETTGKIVPSTNGISNAENSVSQLISRSTD  512
Db   1456 -RTDKALTPVSLSAVSRTQATGNAIS------SAATGLDFVSSDKRLEAASHPTSSLALTSPD 1511

Qy    513 ------------STLRALETVKKVGKVGANGQNAAG---PSADSVTENKIGSPPKT  553
Db   1512 LSGPPGFQSLPASPAPTIRGRGRGRSRGAGRGRRVEGVLHGSNSSITQR-----  1563

Qy    554 PVSNVAATISAGPSNVGTELNSVPQKSSPPLTRVP---------VYPPHS-----  593
Db   1564 --TETATSLASDAEATKF-ALPRSASEIVSRVPKANEGGSTSNPDQVSPVHSATTALRSD 1619

Qy    594 ENIQYFQDPRTQIPFEVPQYP----------QTGYYPPPPTVP-  626
Db   1620 KAADKDLDAPPGFDSGSHVQTLNVLIENSSERKAFAVKKRPLIQGVSSOHPGPNKQPLDLP 1679

Qy    627 -------AGVAPCVPRFVRSNNVPESSLPPASMPY-ADHYSTFSPRDR---  673
Db   1680 VSTSSTLLGGGPVQNQNAVSSVCDGSKSPSEGRTYTALQGVTTAPSDATLPMSSQPSDAT 1739

Qy    674 -PPPQPYGP---------VPPVPESGMYAPVYDSRRIWRPPMY---QRDDIIRSNSLLPM  720
Db   1740 LPMSSQPVGSTVEAQEANVPSLPAALPA---KRRVRNLPSRGETPKRQGKRCQPLPAT 1795

Qy    721 DVMHSSVYQTSL-----RERYNSLDG-----YYSVACQPPSERTTVPLPREPCGHLKTSCE  772
Db   1796 DA--SSARSTGLTPQIEVKVGNLSGTKAKFDAVAKEQPHFSQSVA-----PDIHSSGSLS 1848

Qy    773 EQIRR------                          KPDQWAQYHTQKAPLVSSTLPVATQSPTPPSP-  809
Db   1849 QEIRRDTSGTGGSSARKQTADVTDVARVMKEIFSETSLLKHKVGEPSATTRTNVPDAQSPG 1908

Qy    810 ---LFSVDFRADFSESVSGTKFEE-----       DHLSHYSPWSCGTIGSCINAIDSE  854
Db   1909 EMNLHTVETHK--AEDSSGLKNQEALYNLSKADKLVSDIPHPVPGDLITTSGSVAN----  1961

Qy    855 PKDVIANSNAV-----LMDLDSGDVKRRV---HLFET------QRRTKEE  890
Db   1962 -KDVDIGSSKVAAENELVKIPGGDVDSSVIQLSLGNTLTAKSSLEKCTADQLLGEKLSQE 2020

Qy    891 DPIIPFSDGPIISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSR  950
Db   2021 GETTPASDGETCHL--ABETASSLSYRSEP---TASASTTAEPLPTDKLEKNISFQDE- 2074

Qy    951 WSSYGNEATSSAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALA 1010
Db   2075 ------------VKTLNGDKREAI---LISSE-EQTNVNSKI---ETNSEE 2106

Qy   1011 MQQKWNSLDEGRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPD 1070
Db   2107 LQA--SRTDEVPHVD-----GKSVDVANQTVKED-----EAKHSVEIQSSMLEPDELP 2152

Qy   1071 GQSEPIEEILDIQ-LGISSQNDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEE 1129
Db   2153 NAGQKGHSSIDLQPLVLVTSNE---NAMSLDD-------KDVDPISKSADIEQD 2196

Qy   1130 QKTILPVTSCFSQPLPVSISNASCLPITTSVSAGN---LILKTHVMSEDKNDFLKPVANG 1186
Db   2197 ------PEESVFVQ-----GVGRPKVGTADTQMEDTNDAKLLVGCSVESEEKEKTLQSLIPG 2247

RESULT 6
US-10-559-415-190
; Sequence 190, Application US/10559415
; Publication No. US20060100132A1
; GENERAL INFORMATION:
;  APPLICANT: AstraZeneca AB et al
;  TITLE OF INVENTION: Diagnostic Method
;  FILE REFERENCE: 101073-1P WO
;  CURRENT APPLICATION NUMBER: US/10/559,415
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;  CURRENT FILING DATE: 2005-12-06
;  PRIOR APPLICATION NUMBER: 0313081.2
;  PRIOR FILING DATE: 2003-06-06
;  NUMBER OF SEQ ID NOS: 191
;  SOFTWARE: Patentin version 3.2
;  SEQ ID NO 190
;  LENGTH: 1809
;  TYPE: PRT
;  ORGANISM: Homo Sapiens - peptide sequence of amino acids
US-10-559-415-190

Query Match       2.6%;   Score 159.5;  DB 6;   Length 1809;
Best Local Similarity  19.1%;  Pred. No. 0.33;
Matches 246;  Conservative 174;  Mismatches 429;  Indels 437;  Gaps 66;

Qy    48  KACPFDQTAINTDIDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLAL  107
Db   351  ................RQIKD--TVTMDAGRANKEVEILRKQCKALCQ  397

Qy   108  YLKPLSGGKGVASLNQS------......ALSRPMQRKLVTLVNCQLVEEGRVRAM----RA  154
Db   398  ELKEALQEADVAKCRRDWAFQERDKIVAERDSIRTL------CDNLRRE-RDRAVSELAEA  451

Qy   155  ARSLGE----......RTVTELILQHQNPQQLSANLWAAVRARGCQFLGPAMQEEALKLVL  205
Db   452  LRSLDDTRKQNDVSRELKEL----......KEQMESQLEKEARFR--QLMAHSHDSAIDTDS  503

Qy   206  LALE------......DGSALSRKVLVLFVVQRL-EPRFPQ----......ASKTSIGHVVQLLYRASC  251
Db   504  MEWETEVVEFERETEDIDLKALGFDMAEGVNEPCFPGDCGIFVTKVDKGSIADGRLRVND  563

Qy   252  FKVTKRDEDSSLMQLKEEFRSYEAL------......RREHDAQIV---HIAM----EA  291
Db   564  WILRINDVD--......LINKDKKQAIKALLNGEGAINMVVRRKSLGGKVVTPLHINLSGQKDS  620

Qy   292  GLRISPEQW-SSLLYGDLAHKSHMQSIIDKLQSPESFA--......KSVQELTIVLQRTGDPANL  347
Db   621  GISLENGVYAAAVLPGSPAAKEGSLAVGDRIVAINGIRALDNKSLNECESLLRSCQDSLTL  680

Qy   348  NRLRPHLELLANIDPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQP  407
Db   681  SLLK------......VFPQ----......SSSW----......SGQNIFENIKDSDKMLSFRAH-GPEVQA  719

Qy   408  NSK--......YKTSMCRDLRQQGGCPRGTNCTFAHSQEELEKYRLRNKKINAT  453
Db   720  HNKRNLIQHHNSTQTDIFYTDRLEDRKEPG--......PPGGSSSFLH  759

Qy   454  VRTFPLLNKVGVNNTVTTIAGNVISIGSTETTGKIVPSTNGISNAENSVSQLISRSTDS  513
Db   760  -KPFP----......GGPLQVCPQACPSA---......SERSLSSFRSDASGD  792

Qy   514  TLRALETVK---......KVGKVGANGQONAAGPSADSVTENKIGSPPKTPVSNVAATSA  563
Db   793  RGFGLVDVRGRRPLLPPETEVGGPCGVG--......EASLDKADSEGSNSGGTWPKAMLSSTA----  846

Qy   564  GPSNVGTELNSVPQKSSPFLTRVPVPYPHSENIQYFQDPRTQIPFEVPQY-PQTGY----  618
Db   847  ......-VPEKLS---......VYKKPKQRKSIF-DPNT--......FKRPQTPKIDYLLPG  884

Qy   619  ......-YPPPPTVPAG--VAPCVPRFVPRSNNV---......PESSLP  648
Db   885  PGPAHSPQPSKRAGPLTPPKPKPR--RSDSIKFQHRLETSSESEATLVGSSSPSTSPPSALP  942

Qy   649  P---......ASMPYADHIYSTFSP---......RDR  666
Db   943  PDVDPGEPMHASPPRKARVRIASSYYPEGDGDGSSHLPAKKSCDEDLTSQKVDELGQKRR  1002

Qy   667  MNSSP-YQP---......PPPQPVGPVPVPFSGMYAPVYDSRRI  700
Db  1003  PKSAPSFPRKLAPVVIPAQQFLEEQKCVPASGELSPELQEWAP---......YSPGHSSRHS  1054

Qy   701  WRPPMYQRDDIIRSNSLPPMDVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLP  760
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Query Match       2.6%;   Score 159.5;  DB 6;   Length 1919;
Best Local Similarity  19.1%;  Pred. No. 0.36;
Matches 246;  Conservative 174;  Mismatches 429;  Indels 437;  Gaps 66;

Db  1055  -NPPLYPSRP--SVGTVPRSLITPSTTVSdILRNPIYTVRSHRVGPCSSPPAARDAGPQG  1110
Qy   761  REPCGHLKTSCEEQIRRKPD----QWAQVHTQKAPLVSSTLPVATQSPTPPSPLFSVDFR  816

Db  1111  LHP-----SVQHQGRLSLDL.SHRTCSDYSEMRATHGSNSLPSSARLGSSS---NLQFK  1160
Qy   817  AD------......FSESVSGTKFEEDHLSH----......YSPWSCGTIGSCINAIDSE---PKD  857

Db  1161  AERIKIPSTPRYPRSVVGS--ERGSVSHSECSTPPQSPLNIDTLSSCSGSQSTSASTLPR-  1217
Qy   858  VIANSNAVILMDLDSGGDVKRRVHLFETQRRTKEEDPIIPF----......SDGPIISKWGAIS  909

Db  1218  -IAVNPASL----GERRKDRPYVEEPRHVKVQKGSEPLGISIVSGEKGGIYVSKVTVGS  1271
Qy   910  RSSRTGYHTTDPV----......QATASQ----GSATKPISV-SDYVPYVNAVDSRWSSY  954

Db  1272  IAHQAGLEYGDQLLEFNGINLRSATEQQARLIIGQQCDTITTILAQYNPHVHQLSS----  1326
Qy   955  GNEATSSAHYVERDRFIVTDLLSGHR--KHSSTGDLLSLELQQ-----AKSNSLILQREA  1006

Db  1327  --HSRSSSHLDPAGTHSTLQGSGTTTPEHPSVIDPL-MEQDEGPSTPPAKQSSSRIAGDA  1383
Qy  1007  NALAMQQ-----KKNSLDEGRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDR-----  1055

Db  1384  NKKTLEPRVVFIKKSQLELGVHLC----......GGNLHGVFVAEVEDDSPAKGPDGLV  1432
Qy  1056  --DIELELSALDTDEPDGQSPIEEI  1079

Db  1433  PGDLILEYGSLDV----RNKTVEEV  1453

Qy    48  KACPFDQTAINTDIDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLAL  107
Db   461  KSSTSEKKAANEMEAL----......RQIKD--TVTMDAGRANKEVEILRKQCKALCQ  507

Qy   108  YLKPLSGGKGVASLNQS------......ALSRPMQRKLVTLVNCQLVEEGRVRAM----RA  154
Db   508  ELKEALQEADVAKCRRDWAFQERDKIVAERDSIRTL------CDNLRRE-RDRAVSELAEA  561

Qy   155  ARSLGE----......RTVTELILQHQNPQQLSANLWAAVRARGCQFLGPAMQEEALKLVL  205
Db   562  LRSLDDTRKQNDVSRELKEL----......KEQMESQLEKEARFR--QLMAHSHDSAIDTDS  613

Qy   206  LALE------......DGSALSRKVLVLFVVQRL-EPRFPQ----......ASKTSIGHVVQLLYRASC  251
Db   614  MEWETEVVEFERETEDIDLKALGFDMAEGVNEPCFPGDCGIFVTKVDKGSIADGRLRVND  673

Qy   252  FKVTKRDEDSSLMQLKEEFRSYEAL------......RREHDAQIV---HIAM----EA  291
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RESULT 8
US-11-293-697-3230

Query Match     2.6%;  Score 159;  DB 7;  Length 1057;
Best Local Similarity   19.6%;  Pred. No. 0.17;
Matches 146;  Conservative 100;  Mismatches 264;  Indels 234;  Gaps 36;
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Db    674  WLLRINDVD--LINKDKQAIKALLNGEGAINMVVRRRKSLGGKVVTPLHINLSGQKDS   730
Qy    292  GLRISPEQW-SSLLYGDLAHKSHMQSIIDKLQSPESSPA------KSVQELTIVLQRTGDPANL   347
Db    731  GISLENGVYAAAVLPGSPAAKEGSLAVGDRIVAINGILALDNKSLNECESLLRSCQDSITL   790
Qy    348  NRLRPHLELLANIDPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQP   407
Db    791  SLLK------VFPQ----SSSW------SGQNIFENIKDSDKMLSFRAH-GPEVQA   829
Qy    408  NSK------YKTSMCRDLRQQGGCPRGTNCTFAHSQEELEKYRLRNKKINAT   453
Db    830  HNKRNLIQHNNSTQTDIFYTDRLEDRKBPG--PPGGSSSFLH   869
Qy    454  VRTFPLLNKVGVNNTVTTAGNVISVIGSTETTGKIVPSTNGISNAENSVSQLISRSTDS   513
Db    870  -KPFP------GGPLQVCPQACPSA----SRSLSSFRSDASGD   902
Qy    514  TLRALETVK-------KVGKVGANGQNAAGPSADSVTENKIGSPPKTPVSNVAATSA   563
Db    903  RGFGLVDVGRGRRPLLPPETEVGPCGVG--EASLDKADSEGSNSGGTWPKAMLSSTA---   956
Qy    564  GPSNVGTELNSVPQKSSPFLTRVPVPYFPPHSENIQYFQDPPRTQIPFEVPQY-PQTGY   618
Db    957  -------VPEKLS------VYKKPQKRSIF-DPNT---FKRPQTPKIDYLLPG   994
Qy    619  ----YPPPPTVPAG--VAPCVPRFVRSNNV--------PESSLP   648
Db    995  PGPAHSPQPSKRAGPLTPPKPPR--RSDSIKPQHRLETSSESSEATLVGSSPSTSPPSALP   1052
Qy    649  P----------------ASMPYADHYSTFSP--------RDR   666
Db   1053  PDVDPGEPMHASPPRKARVRIASSYYPEGDGDSSHLPAKKSCDEDLTISQKVDELGQKRR   1112
Qy    667  MNNSSP-YQP------------PPPOPYGPVPPVPESGMYAPVYDSRRI   700
Db   1113  PKSAPSFRPKLAPVVIPAQFLEEQKCVPASGELSPELGEWAP-------YSPGHSSRHS   1164
Qy    701  WRPPMYIQRDDIIRSNSLPPMDVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRITVPLP   760
Db   1165  -NPPLYPSRP----SVGTVPRSLTPSTTVSSILRNPIYTVRSHRVGPCSSPPAARDAGPQG   1220
Qy    761  REPCGHLKTSCEEQIRRKPD-----QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFR   816
Db   1221  LHP------SVQHQGRLSLDLSHRTCSDYSEMRATHGSNSLPSSAARLGSSS----NLQFK   1270
Qy    817  AD-------FSESVSGTKFEEDHLSH-----YSPWSCGTIGSCITNAIDSE---PKD   857
Db   1271  AERIKIPSTPRYPRSVVGS--ERGSVSHSECSTPPQSPLNIDTLSSCSQSQTSASTLPR-   1327
Qy    858  VIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPF------SDGPIISKWGAIS   909
Db   1328  -IAVNPASL-----GERRKDRPVVEEPRHVKVQKGSEPLGISIVSGEKGGIYVSKVTVGS   1381
Qy    910  RSSRTGYHTTDPV--------QATASQ------GSATKPISV-SDYVPYVNAVDSRWSSY   954
Db   1382  IAHQAGLEYGDQLLEFNGINLRSATEQQOARLIIGQQCDTITILAQYNPHVHQLSS----   1436
Qy    955  GNEATSSAHYVERDRFIVTDLSGHR-----KHSSTGDLLSLELCQ----AKSNSLLLQREA   1006
Db   1437  --HSRSSHLDPAGTHSTLQGSGTTTPEHPSVIDPL-MEQDEGPSTPAKQSSSRIAGDA   1493
Qy   1007  NALAMQQ----KWNSLDEGRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDR-----   1055
Db   1494  NKKTLEPRVVFIKSQLELGVHLC----GGNLHGVVAEVEDDSPAKGPDGLV   1542
Qy   1056  --DIELELSALDTDEPDCGSEPIEEI   1079
Db   1543  PGDLILEYGSLDV-----FNKTVEEV   1563

Qy    554  PVSNVAATSA------------------------------GPSNVGTELNS-------V   575
Db      3  PLRSVASTSAKNDLDLNRSQTGKDCHLHRHFVDPVLNQLQRPQETGERLNKYKEEHRRI   62
Qy    576  PQKS---------SPFLTRVPVPYFPPHSENIQYF--------QDPRTQI   611
Db     63  LQESIDVARFTTKIKGLEGERENYSRVASSSSSPKSHIIKQDMDVERSVSDLIYKMKHSVP   122
Qy    612  Q-YPQTGYYPPPPTVPPAGVAPCVPRFVRSNNVPESSLPPAASMP   663
Db    123  QSLPQSNYFT----------TLSNSVVNE--PPRSYPSKEVSNIIYGDKQSNALA   164
Qy    664  RDRMN--------SSPYQPP----PQPYGPVPPVPSGMYAP------VYDSRRIWRPPM   705
Db    165  AAAANPQTLITSFITSLSKPPPLIKHQPESEVGKIPE--HLPHQIASHSVTTFRNDCRSPT   222
Qy    706  YQRDDIIRSNSLPPMDVMH-SSVYQTSLRERYNSLDGYYSVACQPPS-------   751
Db    223  HL--TVSSTNTLRSMPALIRAPVFHPPIIHSLERKEGSYS-SLSPPTLTPVMPVNAGGKV   279
Qy    752  -----EPRTTVPLPREPCGHLKTSCEEQIRRKPDQW-----------AQYHTQK-   791
Db    280  QESQKPPTLIPEPKDSQANFKSSSEQSL---TEMWRPNNNLSKEKTEWHVEKSSGKLQAA   336
Qy    792  LVSSTLPVATQSPTPPSPLFSVDRRADFSEBVSGTKFEEDHLSHSPWSCGTIGSCINAI   851
Db    337  MASVIVRPSSSTKTDSMPAMQLASKDRVSERSSAGAHKTDCLKLAEBAGETGRI--ILPNV   394
Qy    852  DSEPKDVIANSNAVLMDLDSGDVKRRV-HLFETQRRTKEEDPIIPFSDGPIISKWGAISR   910
Db    395  NSD--SVHTKSEKNFQAVSGQSVPPSSVMSAVNTMCNTK-TDVITSAADTTSVSSWCG---   448
Qy    911  SSRTGYHTTDPVQATASQSQSATKPIS-----VSDYVPYVNAVDSRWSSYGNEATS   960
Db    449  SEVTTSLSNTILASTSSECVSSKSVSQPVAQOKQECKVSTTAPVTLAS---SKTGSVQP   504
Qy    961  SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELCQQRKANSNSLLLQREANALAMQQOKWNSLDE   1020
Db    505  SSGFSG----TTDFIHLKGHKA------ALAAAQYKSSN-ASETEPNAIKNQTLSASLPL   553
Qy   1021  GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSAL------DTDEPDGQ   1072
Db    554  DSTVICSTINKANSVGNGQA-----SQTSQPNYHTKLKKAWLTRHSEEDKNTNKMENS   606
Qy   1073  SEPIEEIL------DIQLGISGQ------NDQLLN   1098
Db    607  GNSVSEIIKPCSVNLIASTSSDIQNSVDSKIIVDKYVKDDKVNRRKAKRTYESGSESGDS   666
Qy   1099  VENGHPVQQHQKEPPK-----QKKQS   1119
Db    667  DESESKSEQRTKRQPKPTYKKKQN   690
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RESULT 9
US-10-953-349-13469
Sequence 13469, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
  APPLICANT: ALEXANDROV, Nickolai et al.
  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
  TITLE OF INVENTION: ENCONDED THERBY
  FILE REFERENCE: 2750-1579PUS2
  CURRENT APPLICATION NUMBER: US/10/953,349
  CURRENT FILING DATE: 2004-09-30
  NUMBER OF SEQ ID NOS: 40252
  SOFTWARE: Patentin version 3.3
SEQ ID NO 13469
  LENGTH: 443
  TYPE: PRT
  ORGANISM: Glycine max
US-10-953-349-13469

Query Match   2.6%;   Score 158.5;   DB 6;   Length 443;
Best Local Similarity   21.5%;   Pred. No. 0.054;
Matches 104;   Conservative   42;   Mismatches 154;   Indels 183;   Gaps 22;

Qy   434 AHSQEELEKYRLRNKKIINATVRTFPLLNKVGVNNTVTTIAGNVISVIGSTETTGKIVPST 493
                |::|:|:||:|:|:||||||||||||||||||||||||||||::|:||:::
Db   67 AETQKELAKLQLAQKESSS------------------------------------SS 87

Qy   494 NGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQ------------NAAGPSA 539
                |:||||||||||||||||||||||||||||||||||| |||||
Db   88 HSQSNEERSSPTTDPKKTDNA----------------------SDANNQQLALALPHQIAPQPQPAAPSA 135

Qy   540 DSVTENKIGSP---------PKTPVSNVAATSAGPSN---VGTELNSVPQKSSPFLTRVPVY 589
                ::::   :::
Db   136 QAAASNVTQAPQQPPYYIPPTMPN-SALPQHPQNQYLPSDQQYRTPQLVAPQPTPSQVT 194

Qy   590 P-PHSENIQYFQDPRTQIPFEVPQYPQTGY-----YPPP-----PTVPAGVAPCVPR 635
                 :::| |||
Db   195 PSPPVQQFSHYQQPQQQ--QQPPQQQQQQWSQQVQPSQPPPMQSQVRPSSPNVYPPYQPN 252

Qy   636 FVRSNNVPESSLPPASMPYADHYSTFSPR---DRMNSSPY---------QPPPQPYGP 682
                ::| ||||
Db   253 --QATNPSPAETLPNSMAMQMPYSGVPQQGSNRADAIPYGYGGAGRTVPQQPPPQQMKSS 310

Qy   683 VPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQTSLRERYNSLDGY 742
                |||
Db   311 FPAPPGEMYGP--------------------------TGSLPALPPPSSA--------YMMYDGE 341

Qy   743 YSVACQPPSEPR------------TTVPLPREPCGHLKTSCEEQIRRKPD---QWAQYHTQKAPL 792
                                     |||
Db   342 GGRSHHPQPPHFAQPGYPPTSASLQNPPQGH-----NLMVRNPNQSQFVRNHPYNELI 395

Qy   793 VSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEE------------DHLSHYSP--- 838
                                                           |||
Db   396 -------------------EKLVSMGFRGDHVASVI-QRMEESGQAVDFNSVLDRLSSVGPQRG 439

Qy   839 -WS 840
Db   440 GWS 442

RESULT 10
US-10-953-349-13468
Sequence 13468, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
  APPLICANT: ALEXANDROV, Nickolai et al.
  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
  TITLE OF INVENTION: ENCONDED THERBY
  FILE REFERENCE: 2750-1579PUS2
  CURRENT APPLICATION NUMBER: US/10/953,349
  CURRENT FILING DATE: 2004-09-30
  NUMBER OF SEQ ID NOS: 40252
  SOFTWARE: Patentin version 3.3
SEQ ID NO 13468
  LENGTH: 451
  TYPE: PRT
  ORGANISM: Glycine max
US-10-953-349-13468

Query Match   2.6%;   Score 158.5;   DB 6;   Length 451;
Best Local Similarity   21.5%;   Pred. No. 0.056;
Matches 104;   Conservative   42;   Mismatches 154;   Indels 183;   Gaps 22;

Qy   434 AHSQEELEKYRLRNKKIINATVRTFPLLNKVGVNNTVTTIAGNVISVIGSTETTGKIVPST 493
                |::|:|:||:|:|:||||||||||||||||||||||||||||::|:||:::
Db   75 AETQKELAKLQLAQKESSS------------------------------------SS 95

Qy   494 NGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQ------------NAAGPSA 539
                |:||||||||||||||||||||||||||||||||||| |||||
Db   96 HSQSNEERSSPTTDPKKTDNA----------------------SDANNQQLALALPHQIAPQPQPAAPSA 143

Qy   540 DSVTENKIGSP---------PKTPVSNVAATSAGPSN---VGTELNSVPQKSSPFLTRVPVY 589
                ::::
Db   144 QAAASNVTQAPQQPPYYIPPTMPN-SALPQHPQNQYLPSDQQYRTPQLVAPQPTPSQVT 202

Qy   590 P-PHSENIQYFQDPRTQIPFEVPQYPQTGY-----YPPP-----PTVPAGVAPCVPR 635
                 :::| |||
Db   203 PSPPVQQFSHYQQPQQQ--QQPPQQQQQQWSQQVQPSQPPPMQSQVRPSSPNVYPPYQPN 260

Qy   636 FVRSNNVPESSLPPASMPYADHYSTFSPR---DRMNSSPY---------QPPPQPYGP 682
                ::| ||||
Db   261 --QATNPSPAETLPNSMAMQMPYSGVPQQGSNRADAIPYGYGGAGRTVPQQPPPQQMKSS 318

Qy   683 VPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQTSLRERYNSLDGY 742
                |||
Db   319 FPAPPGEMYGP--------------------------TGSLPALPPPSSA--------YMMYDGE 349

Qy   743 YSVACQPPSEPR------------TTVPLPREPCGHLKTSCEEQIRRKPD---QWAQYHTQKAPL 792
                                     |||
Db   350 GGRSHHPQPPHFAQPGYPPTSASLQNPPQGH-----NLMVRNPNQSQFVRNHPYNELI 403

Qy   793 VSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEE------------DHLSHYSP--- 838
                                                           |||
Db   404 -------------------EKLVSMGFRGDHVASVI-QRMEESGQAVDFNSVLDRLSSVGPQRG 447

Qy   839 -WS 840
Db   448 GWS 450

RESULT 11
US-10-953-349-13467
Sequence 13467, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
  APPLICANT: ALEXANDROV, Nickolai et al.
  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
  TITLE OF INVENTION: ENCONDED THERBY
  FILE REFERENCE: 2750-1579PUS2
  CURRENT APPLICATION NUMBER: US/10/953,349
  CURRENT FILING DATE: 2004-09-30
  NUMBER OF SEQ ID NOS: 40252
  SOFTWARE: Patentin version 3.3
SEQ ID NO 13467
  LENGTH: 456
  TYPE: PRT
  ORGANISM: Glycine max
US-10-953-349-13467

Query Match   2.6%;   Score 158.5;   DB 6;   Length 456;
Best Local Similarity   21.5%;   Pred. No. 0.057;
Matches 104;   Conservative   42;   Mismatches 154;   Indels 183;   Gaps 22;

Qy   434 AHSQEELEKYRLRNKKIINATVRTFPLLNKVGVNNTVTTIAGNVISVIGSTETTGKIVPST 493

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Db    80  AETQKELAKLQLAQKESSS                                            100
          :|:|:|:|:|  :|:
Qy   494  NGISNAENSVSQLISRSTDSTLRALETVKVGKVGANGQ------NAAGPSA            539
Db   101  HSQSNEERSSPPTDPKKTDNA------SDANNQQLALALPHQIAPQPQPAPSA          148
Qy   540  DSVTENKIGSP------PKTPVSNVAATSAGPSN---VGTELNSVPQKSSPFLTRVPVY     589
Db   149  QAAASNTQAPQQPPYYIPPTPMPN-SALPQHPQNQYLPSDQQYRTPQLVAPQPTSQVT      207
Qy   590  P-PHSENIQYFQDPRTQIPFEVPQYPQTGY------YPPP---PTVPAGVAPCVPR        635
Db   208  PSPPVQQFSHYQPQQ--QQPPQQQQWSQOQVQPSQPPPMQSQVRPSSPNVYPYQPN        265
Qy   636  FVRSNNVPESSLPPASMPYADHYSTFSPR--DRMNSSPY------QPPPQPYGP          682
Db   266  --QATNPSPAETLPNSMAMQMPYSGVPPQGSNRADAIPYGYGGAGRTVPQQPPPQQMKSS    323
Qy   683  VPPVPSGMYAPVYDSRRIWRPPMYQRDIIRSNSLPPMDVMHSSVYQTSLRERYNSLDGY     742
Db   324  FPAPDGEMYGP------TGSLPALPPPSSA------YMMYDGE                     354
Qy   743  YSVACQPPSEPR------TTVPLPREPCGHLKTSCEEQIRRKPD------QWAQYHTQKAPL  792
Db   355  GGRSHHPPQPHPAPQPGYPPTSASLQNPPQGH------NLMVRNPNQSQFVRNHPYNELI    408
Qy   793  VSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEE------------DHLSHYSP---  838
Db   409  ------------EKLVSMGFRGDHVASVI-QRMEESGQAVDFNSVLDRLSSVGPQRG       452
Qy   839  -WS  840
Db   453  GWS  455
```

RESULT 12
US-10-953-349-16346
Sequence 16346, Application US/10953349
Publication No. US20060107345A1
;   GENERAL INFORMATION:
;   APPLICANT: ALEXANDROV, Nickolai et al.
;   TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
;   FILE REFERENCE: 2750-1579PUS2
;   CURRENT APPLICATION NUMBER: US/10/953,349
;   CURRENT FILING DATE: 2004-09-30
;   NUMBER OF SEQ ID NOS: 40252
;   SOFTWARE: Patentin version 3.3
;   SEQ ID NO 16346
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Glycine max
US-10-953-349-16346

Query Match   2.5%; Score 158; DB 6; Length 240;
Best Local Similarity   26.0%; Pred. No. 0.025;
Matches   73; Conservative 13; Mismatches 103; Indels 92; Gaps 14;

```
Qy   537  PSADSVIENKIGSPPKTPVSNVAATSAGPSNVGTELNSVP-------QKSSPFLTRVPVYPPHS  593
Db    17  PPPSPSPTYYKSPPPPPYYKSPPPPPYYKSPPPPSPTPYYYKSPPPPKEHVHPPY-          75
Qy   594  ENIQYFQDPRTQIPFEVPQYPQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMP       653
Db    76  ----YYHSPPPSPSPPPPY----YYKSPP--PPSPSPPPYYYKSPPPPSPSPPP--P         122
Qy   654  YADHYSTFSPRDRMNSSPYQPPPPQPY---GPVPPVPSGMYAPVYDSRRIWRPPMYQRDD      710
Db   123  YYYH----SP------PPSPSPSPSPYYKSPPPSPSP------------PPPYYYQ-         158
Qy   711  IIRSNSLPPMDVMHSSVYQTSLRERYNSLDGYIYSVACQPPSEPRTTVPLPREPCGHLKTS     770
```

```
Db   159  ----SPPPPSPTSHPPYYKS-----------PP--PPTSYPPP----------            185
Qy   771  CEEQIRRKPDQWAQYH--TQKAPLVSSTLPVATQSPTPPSP                         809
Db   186  -------------PYHYVSPPPPSPSPSPPPYHYTSPPPPSP                        213
```

RESULT 13
US-10-505-928-799
Sequence 799, Application US/10505928
Publication No. US20060088532A1
;   GENERAL INFORMATION:
;   APPLICANT: Ludwig Institute for Cancer Research et al.
;   TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
;   FILE REFERENCE: 28967/39178
;   CURRENT APPLICATION NUMBER: US/10/505,928
;   CURRENT FILING DATE: 2004-08-27
;   PRIOR APPLICATION NUMBER: US 60/363,019
;   PRIOR FILING DATE: 2002-03-07
;   NUMBER OF SEQ ID NOS: 866
;   SOFTWARE: Patentin 3.2
;   SEQ ID NO 799
;   LENGTH: 1384
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-505-928-799

Query Match   2.5%; Score 153; DB 6; Length 1384;
Best Local Similarity   20.7%; Pred. No. 0.52;
Matches 158; Conservative 100; Mismatches 314; Indels 190; Gaps 32;

```
Qy   492  SPPKTPVSNVAATS-------AGPSNVGTELNSVPQKSSPFLTRVPVYPPHSENIQ          549
Db   183  ATRGPS-ACASHSSLVS-SIEKDLQEIMDSLVLEEPGAAGKKPAATSPLSPMANGGRYLL      240
Qy   549  STNGISNAENSVSQLISRSTDSTLRALETVKVGKVGANGQNAAGPSADSVTEN--KIG        597
Db   241  SPPTSPGAMSVGSSYENTSPAFSPLSSPASSGSCASHSPSGGQEPGQPSVPFLVPARSSSYH    300
Qy   598  YFQDPRTQIP----FEVPQYPQTGYYPPPT-----VPAGVAPCVPRFVRSNNVPE           644
Db   301  LALQPPQOSRPSGARSESPRLSRKGGHERPEPGLRGLLTDSPAATVLAEAR--RATESPR      358
Qy   645  --SSLPPASMPYADHYST---FSPRDRMNSSPYQPPPQPYGPGVPPV-----PSGMYAPV      695
Db   359  LGGGQLPVAISLSEYPASGALSQPTSIPGSKFQPPVPAPRNKIGTLQDRPPSPPREPG        418
Qy   696  DSRRIWRPPMYQR-----DDIIRSNSLPPMDVMHSSVYQTSLRERYNSLDGYSVACQPP       750
Db   419  SERVLTTSPSRQLVGRTFSDGLATRTLQPPE-------SPRLGRRGLD---SMRELPP        466
Qy   751  SEP----RTTVPLPREPCGHLKTSCEEQIRRKPDQWAQYHTQKAPLVSSTLPV---ATQS      803
Db   467  LSPSLSRRALSPLPTRTTPDDPKLNREVAESPRPRRWAA-HGASEDFSLTLGARGRRTRS      525
Qy   804  PTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSCINAIDSEPKDVIANSN      863
Db   526  PSPTLGESLAPHKGSFSGRLS-PAYSLGSLTGASPCQSPCVQRKLSSGDLRVPVTRERKN      584
Qy   864  AVLMDLDSGDVKRVHLFETQRRTKEEDPIIFSDGPIISKWGAISRSRTGYHTTDPVQ         923
Db   585  SITEISDNEDDLIEYHRRQRQERLREQE-------------MERLERQRLETILNLC        628
Qy   924  ATASQ-------GSATKPISVSDYVPYVN-------AVDSRMSSYG-                   955
Db   629  AEYSRADGGPEAGELPSIGEATAALALAGRRPSRGLAGASGRSSEEPGVATQRLWESMER      688
Qy   956  ------NEATSSAHVERDRFIVTDLSGHRKHSST---GDLLSLE------                991
Db   689  SDEENLKECCSSTSTQQE------------HEDAPSTKLQGEVLALEEERAQVLGHVEQLKV    739
Qy   992  ------------LQQAKSNSLLLQ--REANALAMQQKWNSLDEGRHLTLNLLSKEIELRN     1037
```

RESULT 14
US-11-293-697-4492
; Sequence 4492, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4492
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4492

Query Match   19.9%; Score 152; DB 7; Length 950;
Best Local Similarity   19.9%;
Matches 178; Conservative 114; Mismatches 337; Indels 266; Gaps 44;

```
Qy    42 LNKLIHRKACPFD----------QTAINTDIDVLPVNFALLQLVGAQVPDHQSIKLSNIGE---  91
         ::|||                  |: :||: :||  |    :  :  ::
Db   109 VNKLRQEALDLELQMEKOQEIAGKQKEIKDLQIAIDSL-DSKDPKHSHMKAQKSGKBEQQ     167

Qy    92 ---NKHYE----------------VAKKCVEDLALYLKPLSGGKGVASLNQSALSRPMQ---   131
            ::::               |:   |   :   :
Db   168 LDIMNKQYQLESRLDEILSRIAKE-TEEIKDLEEQLTEQQIAAN---EALKKDLEGVIS     223

Qy   132 --RKLVTLVNCQLVEEBEGRVRAMRAARSLGERTVTELILQHONPQQLSANLWAAVRARGC   189
           ||: :                      :
Db   224 GLQEYLGTIKGQATQAQNECRKLRDEKETLLQRLTEV------EQERDQLEI           269

Qy   190 QFLGPAMQEEALKLVILLALEDGSSALSRKVILVLFVVQRLEPRFPQASKTSIGHVVQLLYRA 249
                                                          |||
Db   270 ---VAMDAENMRKELAELE--SALQEQ------HEVNASLQQTQGDLSAYEAEARL        316

Qy   250 SCFKVTKRDEDSSLMQILKEEFRSYEALRR--------EHDAQIVHIAM-EAGLRISPE     298
            ::                                  ::
Db   317 NL----------RDAEANQLKEELEKVTRLTQLEQSALQAELEKERQALKNALGKAQFSEEKE 369

Qy   299 QWSSLIYGDLAH------------KSHMQSIIDKLQSPSFAKSVQELTIVLQ-RTG         342
                                    :::|:                    |::
Db   370 QENSELHAKLKHLQDDNNLLKQQLKDFQNHLNHVVDGLVRPEEVAARVDELRRKLKLGTG    429

Qy   343 D-----PANL----NRLRPHLELLANIDPNPDAVSPTWEQLENAM-VAVKTVVHGLVD      390
                                :
Db   430 EMNIHSPSDVLGKSLADLQKQFSEILARSKWERDEAQVRERKLQEEMALQOEKLATCQEE    489

Qy   391 FIQ-------NYSRKGHETP----------QPQPNSKYKT                         413
         |::                                  ||:
Db   490 FRQACERALEARMNFDKRQHEARIQOMENEIHYLQENLNKSMEIQGLTDIQLQEADEEKE    549

Qy   414 SMCRDLRQQGGGCPRGTNCTFAHSQEE------LEKYRLRNKKINATVRTFPLLNKVGVNNTVT 470
                                           |:
Db   550 RILAQLRE--------LEKKKKLEDAKSQEQVFGLKDKELKLKKAVATSDKLATAELTIAKDQLK 606

Qy   471 TTAGNVISV------IGSTET-TGKIVPSTNGISNAENSVS--QLISRSTDSTLRALET     520
         ||:                |:
Db   607 SLHGTVMKINQERAEELQEAERFSRKAAQAARDLTRAEAEIELLQNLIRQKGEQFR-LEM    665

Qy   521 VRKVGKVGANGQNAAGPSADSVTENK----------------IGSPPKTPVSNVAATSAG-PS 566
                                                   |||
Db   666 EKTGVGTGANSQVLEIEIKLNETMERQRTEIARLQNVLDLTGSDNKGGFENVLEIIAELRR   725

Qy   567 NVGTELNSVPQKSSPFLTRVPVY-----PHSENIQYFQDPRTQ----------            611
Db   726 EVSYQNDYISSMADPFKRRGYWPFWPMPPPPSSKVSSHSSQATKDSGVGLKYSASTVRKPR   785

Qy   612 ---QYPQTGYYPPPPT------------VPAGVAPCVP-RFVRS----NNVPESSL------P 648
Db   786 PGQQDGKEGSQPPPASGYWVYSPIRSGLHKLFPSRDADSGGDSQEBSELDDQEEPPFVPSG    845

Qy   649 PASMPYADHYSTFSPRDRMNSSP-----------YGPVPPVPSG                    689
Db   846 PGYNMY---TVLP-----DGSPVPQGMALYAPPPLPNNSRPLTPGTVVYGPPPAGAPM      896

Qy   690 MYAPVYDSRRIWRPPMYQRDDIIRSNSLP--PMDVMHSSV--YQTSLRERYNSL           739
Db   897 VYGP------PPFNF----SIFPIPMGVLHCNVPEHHNLVSGKTYNSL                934

Db   740 RVKELEQQLQESAREAEMERALLQGEREAERALLQKEQKAVDQ------------LQEKLVALET 792
Qy  1038 GELQSDYTEDA------TDTKPDRDIE-----LELSALDTDEPD---------------GQSPEIEE---- 1078
Db   793 G-IQKERDKEAEALETETKLFEDLEFQQLERESRVEEEBERLAGQGGLLRSKAELLRSIAKR  851
Qy  1079 -----IIDIQLG-ISSQNDQLINGMAVENGHPVQQHQKEPPK                      1114
Db   852 KERLAILDSQAGQIRAQAVQESERLARDKNASLQLLQKEBEK                       893
```

RESULT 15
US-10-953-349-21437
; Sequence 21437, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21437
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21437

Query Match   23.6%; Score 151; DB 6; Length 343;
Best Local Similarity   23.6%;
Matches   87; Conservative   32; Mismatches 131; Indels 118; Gaps 19;

```
Qy   535 AGPSADSVTENKIGSP----------PKTPVSNVAATSAGPSN---VGTELNSVPQKSSPFLT 584
         | ||:  :                  |
Db    31 AAPSAQAAAASNVTQAPQQPPYYIPPTPMPN-SALPQHPQNQYLPSDQQYRTPQLVAPQPT    89

Qy   585 RVPVYP-PHSENIQYFQDPRTQIPFEVPQYPQTQY------------YPPP--------PTVPAGVA 630
                                                         |||
Db    90 PSQVTPSPVQQFSHYQPQQQ--QOPQQQOQQQMQSQOVQPSQQPPMQSQVRPSSPNVYP     147

Qy   631 PCVPRFVRSNNVPESSLPPASMPYADHYSTFSPR--DRMNSSPY------------QPPPP      677
Db   148 PYQPN--QATNPSPAETLPNSMAMQMPYSGVPQQGSNRADAIPYGYGGAGRTVPQQPPPQ    205

Qy   678 QPYGPVPVPSGMYAPVDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQTSLRERYN      737
Db   206 QMKSSFPAPPGEMYGP----------TGSLPALPPPSSA-----YM                 236

Qy   738 SLDGSYYSVACQPPSEPR----------TTTVPLPREPCGHLKTSCEEQIRRKPD--QWAQYHT 787
Db   237 MYDGEGGRSHHPQPPHFAQPGPYPPTSASLQNPPQGH---NLMVRNPNQSQFVRNHP       290

Qy   788 QKAPLVSSTLPVATQSPTPPSPLFSVDRRADFSESVSGTKFEE------------DHLSHY     836
Db   291 YNELI-------------------EKLVSMGFRGDHVASVI-QRMEESQQAVDFNSVLDRLSSV 334

Qy   837 SP----WS                                                        840
Db   335 GPQRGGWS                                                        342
```

Search completed: May 24, 2006, 12:53:48
Job time : 15 secs

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.
Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**
Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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OM protein - protein search, using sw model

GenCore version 5.1.8
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Run on: May 24, 2006, 12:48:59 ; Search time 299 Seconds
                 (without alignments)
                 6082.290 Million cell updates/sec

Title: US-10-619-992-2
Perfect score: 6215
Sequence: 1 MPVQAAQWTEFLSCPICVNE..........MSEDXNDFLKPVANGKMVNS 1191

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues
Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Pending_Patents_AA_Main.*

1: /EMC_Celerra_SIDS3/ptodata/2/paa/PCTUS_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/paa/US066_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/paa/US073_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/paa/US074_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/paa/US075_COMB.pep:*
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10: /EMC_Celerra_SIDS3/ptodata/2/paa/US080_COMB.pep:*
11: /EMC_Celerra_SIDS3/ptodata/2/paa/US081_COMB.pep:*
12: /EMC_Celerra_SIDS3/ptodata/2/paa/US082_COMB.pep:*
13: /EMC_Celerra_SIDS3/ptodata/2/paa/US083_COMB.pep:*
14: /EMC_Celerra_SIDS3/ptodata/2/paa/US084_COMB.pep:*
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18: /EMC_Celerra_SIDS3/ptodata/2/paa/US088_COMB.pep:*
19: /EMC_Celerra_SIDS3/ptodata/2/paa/US089_COMB.pep:*
20: /EMC_Celerra_SIDS3/ptodata/2/paa/US090_COMB.pep:*
21: /EMC_Celerra_SIDS3/ptodata/2/paa/US091_COMB.pep:*
22: /EMC_Celerra_SIDS3/ptodata/2/paa/US092_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID		Description
1	6215	100.0	1191	31	US-10-170-205E-31443	Sequence 31443, A
2	6215	100.0	1191	36	US-10-619-992-2	Sequence 2, Appli
3	6215	100.0	1191	49	US-60-452-680-22109	Sequence 22109, A
4	6215	100.0	1191	49	US-60-453-050-13599	Sequence 13599, A
5	6215	100.0	1191	49	US-60-453-135-13599	Sequence 13599, A
6	6215	100.0	1191	49	US-60-466-412-13599	Sequence 13599, A
7	6207	99.9	1191	36	US-10-619-992-4	Sequence 4, Appli
8	5880	94.6	1137	47	US-60-243-734-16	Sequence 16, Appl
9	5880	94.6	1137	31	US-10-170-205E-29971	Sequence 29971, A
10	5525	88.9	1062	49	US-60-452-680-22108	Sequence 22108, A
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15	4416	71.1	869	24	US-09-488-725A-3499	Sequence 3499, Ap
16	4416	71.1	869	32	US-10-258-898A-3499	Sequence 3499, Ap
17	4416	71.1	869	32	US-10-286-897-3499	Sequence 3499, Ap
18	4066.5	65.4	812	24	US-09-488-725A-3500	Sequence 3500, Ap
19	4066.5	65.4	812	32	US-10-258-898A-3500	Sequence 3500, Ap
20	4066.5	65.4	812	32	US-10-286-897-3500	Sequence 3500, Ap
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22	2685	43.2	1134	51	US-60-710-726-114	Sequence 114, App
22	2685	43.2	1134	52	US-60-732-162-682	Sequence 682, App
24	2681.5	43.1	1133	1	PCT-US02-38445-47	Sequence 47, Appl
25	2665.5	42.9	1125	31	US-10-170-205E-7090	Sequence 7090, Ap
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27	2665	42.9	1132	49	US-60-452-680-20520	Sequence 20520, A
28	2106	33.9	421	1	PCT-US00-30653-280	Sequence 280, Appl
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40	1538	24.7	819	40	US-11-097-143-24915	Sequence 24915, A
41	1538	24.7	819	46	US-60-173-464-20563	Sequence 20563, A
42	1538	24.7	819	46	US-60-191-637-25016	Sequence 25016, A
43	1538	24.7	819	46	US-60-191-681-19706	Sequence 19706, A
44	1492.5	24.0	296	1	PCT-US00-30653-281	Sequence 281, App
45	886	14.3	195	27	US-09-758-461-704	Sequence 704, App

ALIGNMENTS

RESULT 1
US-10-170-205E-31443
; Sequence 31443, Application US/10170205E
; GENERAL INFORMATION:

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; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
; FILE REFERENCE: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3143
;   LENGTH: 1191
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-170-205E-31443

Query Match         100.0%;  Score 6215;  DB 31;  Length 1191;
Best Local Similarity   100.0%;
Matches 1191;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
US-10-619-992-2
Sequence 2, Application US/10619992
; GENERAL INFORMATION:
; APPLICANT: Hefeneider, Steven
; APPLICANT: Merkins, Louise
; APPLICANT: Bennett, Robert
; APPLICANT: Seiss, Donald
; TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene a...
; FILE REFERENCE: 00-617-A
; CURRENT APPLICATION NUMBER: US/10/619,992
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/921,099
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 1191
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-619-992-2

Query Match         100.0%;  Score 6215;  DB 36;  Length 1191;
Best Local Similarity   100.0%;
Matches 1191;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy  181  WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG   240
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Db  901  IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSRWSSYGNEATS  960

Qy  961  SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE  1020

Qy 1021  GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021  GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL  1080

Qy 1081  DIQLGISSQNDQLLNGMAVENGHPVQQHQKEPPKQKQKQSLGEDHVILEEQKTILPVTSCF  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081  DIQLGISSQNDQLLNGMAVENGHPVQQHQKEPPKQKQKQSLGEDHVILEEQKTILPVTSCF  1140

Qy 1141  SQPLPVSISNASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS  1191
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141  SQPLPVSISNASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS  1191
```

RESULT 4
US-60-453-050-13599
Sequence 13599, Application US/60453050

; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13599
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-13599

  Query Match   100.0%; Score 6215; DB 49; Length 1191;
  Best Local Similarity   100.0%; Pred. No. 0;
  Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTD 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTD 60

Qy   61 IDVLPVNFALLQLVGAQVPDHQSIKLSNIGENHYEVAKKCVEDLALYLKPLSGGKGVAS 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 IDVLPVNFALLQLVGAQVPDHQSIKLSNIGENHYEVAKKCVEDLALYLKPLSGGKGVAS 120

Qy   121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANL 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANL 180

Qy   181 WAAVRARGCQFLGPAMQEEALKLVILALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 WAAVRARGCQFLGPAMQEEALKLVILALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240

Qy   241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300

Qy   301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360

Qy   361 DPNPDAVSPTWEQLENAMVAVKTVHGLVDFIQNYSRGHETPQPQPNSKYKTSMCRDLR 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 DPNPDAVSPTWEQLENAMVAVKTVHGLVDFIQNYSRGHETPQPQPNSKYKTSMCRDLR 420

Qy   421 QQGGCPRGTNCTFAHSQEELEKXRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISVI 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 QQGGCPRGTNCTFAHSQEELEKXRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISVI 480

Qy   481 GSTETTGKIVPSTNGISNAENSVSQLISRSTDSTILRALETVKKVGKVGANGQNAAGPSAD 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GSTETTGKIVPSTNGISNAENSVSQLISRSTDSTILRALETVKKVGKVGANGQNAAGPSAD 540

Qy   541 SVTENKIGSPPKIPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPPHSENIQYFQ 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 SVTENKIGSPPKIPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPPHSENIQYFQ 600

Qy   601 DPRTQIPFEVPVQTYGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 DPRTQIPFEVPVQTYGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660

Qy   661 FSPRDRMNSSPYQPPPQPQYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 FSPRDRMNSSPYQPPPQPQYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM 720

Qy   721 DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD 780

Qy   781 QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS 840

Qy   841 CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP 900

Qy   901 IISKWGAISRSRSRRIGYHTTDPVQATASQSSATKPISVSDYVPYVNAVDSRWSSYGNEATS 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 IISKWGAISRSRSRRIGYHTTDPVQATASQSSATKPISVSDYVPYVNAVDSRWSSYGNEATS 960

Qy   961 SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE 1020

Qy   1021 GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL 1080

Qy   1081 DIQLGISSQNDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCF 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 DIQLGISSQNDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCF 1140

Qy   1141 SQPLPVSISNASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS 1191
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 SQPLPVSISNASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS 1191

RESULT 5
US-60-453-135-13599
Sequence 13599, Application US/60453135

; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13599
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-13599

  Query Match   100.0%; Score 6215; DB 49; Length 1191;
  Best Local Similarity   100.0%; Pred. No. 0;
  Matches 1191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTD 60

Db 1081 DIQLGISSQNDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCF 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1081 DIQLGISSQNDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCF 1140

Db 1021 GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 1021 GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL 1080

Db   961 SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQOKWNSLDE 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   961 SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQOKWNSLDE 1020

Db   901 IISKWGIAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSRWSSYGNEATS 960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   901 IISKWGIAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSRWSSYGNEATS 960

Db   841 CGTIGSCTNAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   841 CGTIGSCTNAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP 900

Db   781 QWAQYHTQKAPLVSSTLPVATQSPTPFSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   781 QWAQYHTQKAPLVSSTLPVATQSPTPFSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS 840

Db   721 DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   721 DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD 780

Db   661 FSPRDRMNSSPYQPPPPQPQYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   661 FSPRDRMNSSPYQPPPPQPQYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM 720

Db   601 DPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   601 DPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660

Db   541 SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPYPPHSENIQYFQ 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   541 SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPYPPHSENIQYFQ 600

Db   481 GSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSAD 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   481 GSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSAD 540

Db   421 QQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISVI 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   421 QQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISVI 480

Db   361 DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPQNSKYKTSMCRDLR 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   361 DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPQNSKYKTSMCRDLR 420

Db   301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360

Db   241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300

Db   181 WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   181 WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240

Db   121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAAARSLGERTVTELILQHQNPQQLSANL 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAAARSLGERTVTELILQHQNPQQLSANL 180

Db   61 IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61 IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVAS 120

Db   1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTTCLNKLHRRACPFDQTAINTD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTTCLNKLHRRACPFDQTAINTD 60

RESULT 6
US-60-466-412-13599
Sequence 13599, Application US/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001466
; CURRENT APPLICATION NUMBER: US/60/466,412
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13599
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-466-412-13599

Query Match   100.0%; Score 6215; DB 49; Length 1191;
Best Local Similarity 100.0%;
Matches 1191; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTTCLNKLHRRACPFDQTAINTD 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTTCLNKLHRRACPFDQTAINTD 60

Qy   61 IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVAS 120

Qy   121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAAARSLGERTVTELILQHQNPQQLSANL 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAAARSLGERTVTELILQHQNPQQLSANL 180

Qy   181 WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240

Qy   241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300

Qy   301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360

Qy   361 DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPQNSKYKTSMCRDLR 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPQNSKYKTSMCRDLR 420

Qy   421 QQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISVI 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 QQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISVI 480

Qy   481 GSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSAD 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSAD 540

Qy   541 SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPYPPHSENIQYFQ 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPYPPHSENIQYFQ 600

Qy   601 DPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 DPRTQIPFEVPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660

```
RESULT 7
US-10-619-992-4
Sequence 4, Application US/10619992
GENERAL INFORMATION:
;   APPLICANT: Hefeneider, Steven
;   APPLICANT: Merkins, Louise
;   APPLICANT: Bennett, Robert
;   APPLICANT: Seiss, Donald
;   TITLE OF INVENTION: Mammalian DNA Binding Membrane-Associated Protein-encoding Gene a
;   FILE REFERENCE: 00-617-A
;   CURRENT APPLICATION NUMBER: US/10/619,992
;   CURRENT FILING DATE: 2003-07-15
;   PRIOR APPLICATION NUMBER: US/09/921,099
;   PRIOR FILING DATE: 2001-08-01
;   NUMBER OF SEQ ID NOS: 21
;   SOFTWARE: Patentin version 3.0
;   SEQ ID NO 4
;   LENGTH: 1191
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-619-992-4

Query Match        99.9%;  Score 6207;  DB 36;  Length 1191;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 1190;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
```

RESULT 7 alignment (left/center column):

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Qy     1  MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTCLNKLHRKACPPQTAINTD   60
          ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MAVQAAQWTEFLSCFICYNEFDENVHKPISLGCSHTVCKTCLNKLHRKACPPQTAINTD   60

Qy    61  IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVAS  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVAS  120

Qy   121  LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQOLSANL  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQOLSANL  180

Qy   661  FSPRDRMNSSPYQPPPQPYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM   720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  FSPRDRMNSSPYQPPPQPYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM   720

Qy   721  DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD  780

Qy   781  QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS  840

Qy   841  CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP  900

Qy   901  IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSRWSSYGNEATS  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSRWSSYGNEATS  960

Qy   961  SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE  1020

Qy  1021  GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL  1080

Qy  1081  DIQLGISSQNDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCF  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  DIQLGISSQNDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCF  1140

Qy  1141  SQPLPVSISNASCLPITTSVSAGNLILKTHVMSEDKDNDFLKPVANGKMVNS          1191
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  SQPLPVSISNASCLPITTSVSAGNLILKTHVMSEDKDNDFLKPVANGKMVNS          1191
```

RESULT 8 alignment (right column):

```
Db   121  LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQOLSANL  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   181  WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQQASKTSIG  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  WAAVRARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQQASKTSIG  240

Qy   241  HVQOLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  HVQOLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW  300

Qy   301  SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGPDPANLNRLRPHLELIANI  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGPDPANLNRLRPHLELIANI  360

Qy   361  DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQOPQPNSKXYKTSMCRDLR  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQOPQPNSKXYKTSMCRDLR  420

Qy   421  QOQGCPRGTNCTTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTTYTTTAGNVISVI  480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  QOQGCPRGTNCTTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTTYTTTAGNVISVI  480

Qy   481  GSTETTGKIVPSTNGISNAENSVSQLIRSTDSTLRALETVKKVGKVGANGQNAAGPSAD   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  GSTETTGKIVPSTNGISNAENSVSQLIRSTDSTLRALETVKKVGKVGANGQNAAGPSAD   540

Qy   541  SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPPHSENIQYFQ  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPPHSENIQYFQ  600

Qy   601  DPRTQIPEEVPQYPQTGYYPPPPYPPTPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  DPRTQIPEEVPQYPQTGYYPPPPYPPTPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST  660

Qy   661  FSPRDRMNSSPYQPPPQPYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM   720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  FSPRDRMNSSPYQPPPQPYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM   720

Qy   721  DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  DVMHSSVYQTSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD  780

Qy   781  QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS  840

Qy   841  CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP  900

Qy   901  IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSRWSSYGNEATS  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  IISKWGAISRSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSRWSSYGNEATS  960

Qy   961  SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE  1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE  1020

Qy  1021  GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL  1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEIL  1080

Qy  1081  DIQLGISSQNDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCF  1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  DIQLGISSQNDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCF  1140

Qy  1141  SQPLPVSISNASCLPITTSVSAGNLILKTHVMSEDKDNDFLKPVANGKMVNS          1191
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141  SQPLPVSISNASCLPITTSVSAGNLILKTHVMSEDKDNDFLKPVANGKMVNS          1191
```

RESULT 8

```
US-60-243-734-16
; Sequence 16, Application US/60243734
; GENERAL INFORMATION:
;   APPLICANT: Beasley, Ellen
;   TITLE OF INVENTION: ISOLATED HUMAN PHASE I DRUG-METABOLIZING
;   TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
;   TITLE OF INVENTION: DRUG-METABOLIZING PHASE I PROTEINS, AND USES THEREOF
;   FILE REFERENCE: CL000932
;   CURRENT APPLICATION NUMBER: US/60/243,734
;   CURRENT FILING DATE: 2000-10-30
;   NUMBER OF SEQ ID NOS: 30
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 1137
;   TYPE: PRT
;   ORGANISM: HUMAN
US-60-243-734-16

Query Match          94.6%;  Score 5880;  DB 47;  Length 1137;
Best Local Similarity   95.4%;  Pred. No. 0;
Matches 1136;  Conservative 1;  Mismatches 0;  Indels 54;  Gaps 3;

Qy    1 MPVQAAQWTEFLSCPICYNEFPDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTD   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MPVQAAQWTEFLSCPICYNEFPDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTD   60

Qy   61 IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPILSGGGKGVAS  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPILSGGGKGVAS  120

Qy  121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQOLSANL   180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQOLSANL   180

Qy  181 WAAVRARGCQFLGPAMQEEALKLVILALEDGSALSRKVLVLFVVQRLEPRFPQQASKTSIG   240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 WAAVRARGCQFLGPAMQEEALKLVILALEDGSALSRKVLVLFVVQRLEPRFPQQASKTSIG   240

Qy  241 HVVQLLVRASCRKVTKRDEDDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW   300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 HVVQLLVRASCRKVTKRDEDDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW   300

Qy  301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI   360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI   360

Qy  361 DPNPDAVSPTWEQLENAMAVAKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLR   420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 DPNPDAVSPTWEQLENAMAVAKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLR   420

Qy  421 QGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTAGNVISVI   480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 QGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTAGNVISVI   480

Qy  481 GSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKVGKVGANGQNAAGPSAD   540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GSTETTGKIVPSTNGISNAENSVSQLISRSTDSTLRALETVKVGKVGANGQNAAGPSAD   540

Qy  541 SVTENKIGSPPKPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPPHSENIQYFQ   600
        ||||                             ||||||||||||
Db  541 SVTE--------------------------KVPVYPPHSENIQYFQ              560

Qy  601 DPRTQIPFEVPQYPQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMYADHYST   660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  561 DPRTQIPFEVPQYPQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMYADHYST   620

Qy  661 FSPRDRMNSSPYQPPPQPYGVPVPPVSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM   720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  621 FSPRDRMNSSPYQPPPQPYGVPVPPVSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM   680

Qy  721 DVMHSSVYQTSLRERYNSLDGIYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD   780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  681 DVMHSSVYQTSLRERYNSLDGIYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPD   740

Qy  781 QWAQYHTQKAPLVSSTLPVATQSPTPPPSPLFSVDFRADPSESVSGGTKFEEDHLSHYSPWS   840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  741 QWAQYHTQKAPLVSSTLPVATQSPTPPPSPLFSVDFRADPSESVSGGTKFEEDHLSHYSPWS   800

Qy  841 CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP   900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  801 CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP   860

Qy  901 IISKWGAISRSRSSRTGYHTDPVQATASQGSSAATKPISVSDYVPYVNAVDSRWSSSYGNEATS   960
        ||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db  861 IISKWGAISRSRSSRTGYHTDPVQATASQGSSATKPISVSDVPYVNAVDSRWSSSYGNEATS   920

Qy  961 SAHYVERDRFIVTDLLSGHRKHSSTGDLLSLELQQOAKSNSLLLQREANALAMQQKWNSLDE  1020
        ||||||                  ||||||||||||||||||||||||||||||||||||
Db  921 SAHYVE-------------------RKHSSTGDLLSLELQQOAKSNSLLLQREANALAMQQKWNSLDE   968

Qy 1021 GRHLTLNLLSKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEDPGQSEPIEEIL  1080
        ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db  969 GRHLTLNLLSKEIELRNGE--SDYTEDATDTKPDRDIELELSALDTDEDPGQSEPIEEIL  1026

Qy 1081 DIQLGISSQQNDQLLNGMAVENGHPVQQHQOKEPPRQOKKQOSLGEDHVILEEQKTILPVTSCF  1140
        ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db 1027 DIQLGISSQQNDQLLNGMAVENGHPVQQHQOKEPPKOKKOSLGEDHVILEEQKTILPVTSCF  1086

Qy 1141 SQPLPVSISNASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS  1191
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1087 SQPLPVSISNASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS  1137


RESULT 9
US-10-170-205E-29971
; Sequence 29971, Application US/10170205E
; GENERAL INFORMATION:
;   APPLICANT: ADAMS, Mark
;   TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
;   TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
;   FILE REFERENCE: CL001381
;   CURRENT APPLICATION NUMBER: US/10/170,205E
;   CURRENT FILING DATE: 2002-06-13
;   NUMBER OF SEQ ID NOS: 40312
;   SOFTWARE: Patentin version 3.2
; SEQ ID NO 29971
;   LENGTH: 1062
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-170-205E-29971

Query Match          88.9%;  Score 5525;  DB 31;  Length 1062;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1062;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy  130 MQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQOLSANLWAAVRARGC  189
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQOLSANLWAAVRARGC   60

Qy  190 QFLGPAMQEEALKLVILALEDGSALSRKVLVLFVVQRLEPRFPQQASKTSIGHVVQLLYRA  249
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 QFLGPAMQEEALKLVILALEDGSALSRKVLVLFVVQRLEPRFPQQASKTSIGHVVQLLYRA  120

Qy  250 SCRKVTKRDEDDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLA  309
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SCRKVTKRDEDDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLA  180

Qy  310 HKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANIDPNPDAVSP  369
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 HKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANIDPNPDAVSP  240

Qy  370 TWEQLENAMAVAKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLRQQGGCPRGT  429
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TWEQLENAMAVAKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLRQQGGCPRGT  300

Qy  430 NCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTAGNVISVIGISTETTGKI  489
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 NCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTAGNVISVIGISTETTGKI  430
```

RESULT 10
US-60-452-680-22108
; Sequence 22108, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22108
; LENGTH: 1062
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-22108

Query Match   88.9%;   Score 5525;   DB 49;   Length 1062;
Best Local Similarity   100.0%;   Pred. No. 0;

Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[Sequence alignment data: Qy/Db paired amino-acid sequence blocks with
position numbers from 1 to 1191, rendered with vertical-bar identity
lines between each Query (Qy) and Database (Db) line.]

```
RESULT 11
US-60-453-050-13598
; Sequence 13598, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13598
; LENGTH: 1062
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-13598

Query Match             88.9%;  Score 5525;  DB 49;  Length 1062;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1062;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   130 MQRKLVTLVNCQLVEEGRVRAMRAARSLGERTVTELILLQHQNPQQLSANLWAAVRARGC 189
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MQRKLVTLVNCQLVEEGRVRAMRAARSLGERTVTELILLQHQNPQQLSANLWAAVRARGC  60

Qy   190 QFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQLLYRA 249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 QFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQLLYRA 120

Qy   250 SCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLA 309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLA 180

Qy   310 HKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANIDPNPDAVSP 369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 HKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANIDPNPDAVSP 240

Qy   370 TWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLRQQGCPRGT 429
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLRQQGCPRGT 300

Qy   430 NCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISVISVIGSTETTGKI 489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 NCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISVISVIGSTETTGKI 360

Qy   490 VPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSADSVTENKIGS 549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 VPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSADSVTENKIGS 420

Qy   550 PPKTPVSNVAATSAGPSNVGTELNSVPQKSSPPLTRVPVYPHSENIQYFQDPRTQIPPE 609
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 PPKTPVSNVAATSAGPSNVGTELNSVPQKSSPPLTRVPVYPHSENIQYFQDPRTQIPPE 480

Qy   610 VPQYPQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYSTFSPRDRMNS 669
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 VPQYPQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYSTFSPRDRMNS 540

Qy   670 SPYQPPPPQPYGPVPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQ 729
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 SPYQPPPPQPYGPVPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQ 600

Qy   730 TSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPDQWAQYHTQK 789
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPDQWAQYHTQK 660

Qy   790 APLVSSTLPVATQSPTTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSCIN 849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 APLVSSTLPVATQSPTTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSCIN 720

Qy   850 AIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGPIIISKWGAIS 909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGPIIISKWGAIS 780

Qy   910 RSSRTGYHTTDPVQATASGQSSATKPISVSDYVPYVNAVDSRWSSYGNEATSSAHVERDR 969
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 RSSRTGYHTTDPVQATASGQSSATKPISVSDYVPYVNAVDSRWSSYGNEATSSAHVERDR 840

Qy   970 FIVTDLSGHRKHSSTGDLLSLELQQAKSNJLLLQREANALAMQQKWNSLDEGRHLTLNLL 1029
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 FIVTDLSGHRKHSSTGDLLSLELQQAKSNJLLLQREANALAMQQKWNSLDEGRHLTLNLL 900

Qy  1030 SKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEILIDIQLGISSQ 1089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 SKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEILIDIQLGISSQ 960

Qy  1090 NDQLLNGMAVENGHPVQQHQKEPPKQKQQSLGEDHVILEEQKTILPVTSCFSQPLPVSIS 1149
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 NDQLLNGMAVENGHPVQQHQKEPPKQKQQSLGEDHVILEEQKTILPVTSCFSQPLPVSIS 1020

Qy  1150 NASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS 1191
             ||||||||||||||||||||||||||||||||||||||||||
Db  1021 NASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS 1062


RESULT 12
US-60-453-135-13598
; Sequence 13598, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13598
; LENGTH: 1062
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-13598

Query Match             88.9%;  Score 5525;  DB 49;  Length 1062;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1062;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   130 MQRKLVTLVNCQLVEEGRVRAMRAARSLGERTVTELILLQHQNPQQLSANLWAAVRARGC 189
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MQRKLVTLVNCQLVEEGRVRAMRAARSLGERTVTELILLQHQNPQQLSANLWAAVRARGC  60

Qy   190 QFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQLLYRA 249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 QFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQLLYRA 120

Qy   250 SCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLA 309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLA 180

Qy   310 HKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANIDPNPDAVSP 369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 HKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANIDPNPDAVSP 240

Qy   370 TWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLRQQGCPRGT 429
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLRQQGCPRGT 300

Qy   430 NCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISVISVIGSTETTGKI 489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 NCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISVISVIGSTETTGKI 360

Qy   490 VPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSADSVTENKIGS 549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 VPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSADSVTENKIGS 420
```

RESULT 13
US-60-466-412-13598
Sequence 13598, Application US/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001466
; CURRENT APPLICATION NUMBER: US/60/466,412
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13598
; LENGTH: 1062
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-466-412-13598

  Query Match   88.9%; Score 5525; DB 49; Length 1062;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 1062; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   130 MQRKLVTLVNCQLVEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANLWAAVRARGC 189
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   130 MQRKLVTLVNCQLVEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANLWAAVRARGC 189

Qy   361 VPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGVKVGANGQNAAGPSADSVTENKIGS
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 VPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGVKVGANGQNAAGPSADSVTENKIGS 420

Qy   550 PPKTPVSNVAATSAGPSNVGTELNSVPQKSSSPFLTRVPVYPPHSENIQYFQDPRTQIPFE 609
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 PPKTPVSNVAATSAGPSNVGTELNSVPQKSSSPFLTRVPVYPPHSENIQYFQDPRTQIPFE 480

Qy   610 VPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYSTFSPRDRMNS 669
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 VPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYSTFSPRDRMNS 540

Qy   670 SPYQPPPPPQYGPVPVPPVPGSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQ 729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 SPYQPPPPPQYGPVPVPPVPGSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQ 600

Qy   730 TSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPDQWAQYHTQK 789
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPDQWAQYHTQK 660

Qy   790 APLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSCIN 849
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 APLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSCIN 720

Qy   850 AIDSEPKDVIANSNAVLMDLDSGDVKRVHLFETQRRTKEEDPIIPFSDGPIISKWGAIS 909
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AIDSEPKDVIANSNAVLMDLDSGDVKRVHLFETQRRTKEEDPIIPFSDGPIISKWGAIS 780

Qy   910 RSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSRWSSYGNEATSSAHYVERDR 969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 RSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSRWSSYGNEATSSAHYVERDR 840

Qy   970 FIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDEGRHLTLNLL 1029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 FIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDEGRHLTLNLL 900

Qy   1030 SKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEILDIQLGISSQ 1089
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 SKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEILDIQLGISSQ 960

Qy   1090 NDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCFSQPLPVSIS 1149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 NDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCFSQPLPVSIS 1020

Qy   1150 NASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS 1191
          ||||||||||||||||||||||||||||||||||||||||||
Db   1021 NASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS 1062

RESULT 14
US-10-485-225-8

Db   1 MQRKLVTLVNCQLVEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANLWAAVRARGC 60

Db   190 QFLGPAMQBEALIKLVILLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQLLYRA 249

Db   61 QFLGPAMQBEALIKLVILLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQLLYRA 120

Qy   250 SCFKVTKRDEDSLLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLA 309
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SCFKVTKRDEDSLLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLA 180

Db   310 HKSHMQSIIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANIDPNPDAVSP 369
          HKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANIDPNPDAVSP

Db   181 HKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANIDPNPDAVSP 240

Qy   430 NCTFAHSQEBLEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISIVIGTSTETTGKI 489
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 NCTFAHSQEBLEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISIVIGTSTETTGKI 360

Db   241 TWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETFPQPQPNSKYKTSMCRDLRQQGGCPRGT 300
          TWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETFPQPQPNSKYKTSMCRDLRQQGGCPRGT

Db   361 VPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSADSVTENKIGS 420

Qy   490 VPSTNGISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSADSVTENKIGS 549
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   550 PPKTPVSNVAATSAGPSNVGTELNSVPQKSSSPFLTRVPVYPPHSENIQYFQDPRTQIPFE 609
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 PPKTPVSNVAATSAGPSNVGTELNSVPQKSSSPFLTRVPVYPPHSENIQYFQDPRTQIPFE 480

Qy   610 VPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYSTFSPRDRMNS 669
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 VPQYPQTGYYPPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYSTFSPRDRMNS 540

Qy   670 SPYQPPPPPQYGPVPVPPVPGSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQ 729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 SPYQPPPPPQYGPVPVPPVPGSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQ 600

Qy   730 TSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPDQWAQYHTQK 789
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TSLRERYNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPDQWAQYHTQK 660

Qy   790 APLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSCIN 849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 APLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSCIN 720

Qy   850 AIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGPIISKWGAIS 909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGPIISKWGAIS 780

Qy   910 RSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSRWSSYGNEATSSAHYVERDR 969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 RSSRTGYHTTDPVQATASQGSATKPISVSDYVPYVNAVDSRWSSYGNEATSSAHYVERDR 840

Qy   970 FIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDEGRHLTLNLL 1029
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 FIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDEGRHLTLNLL 900

Qy   1030 SKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEILDIQLGISSQ 1089
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 SKEIELRNGELQSDYTEDATDTKPDRDIELELSALDTDEPDGQSEPIEEILDIQLGISSQ 960

Qy   1090 NDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCFSQPLPVSIS 1149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 NDQLLNGMAVENGHPVQQHQKEPPKQKKQSLGEDHVILEEQKTILPVTSCFSQPLPVSIS 1020

Qy   1150 NASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS 1191
          ||||||||||||||||||||||||||||||||||||||||||
Db   1021 NASCLPITTSVSAGNLILKTHVMSEDKNDFLKPVANGKMVNS 1062

```
Sequence 8, Application US/10485225
GENERAL INFORMATION:
  APPLICANT: Greener, Tsvika
  APPLICANT: Moskowitz, Haim
  APPLICANT: Reiss, Yuval
  APPLICANT: Alroy, Iris
  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
  TITLE OF INVENTION: MODULATION OF VIRAL MATURATION
  FILE REFERENCE: PROL-P02-001
  CURRENT APPLICATION NUMBER: US/10/485,225
  CURRENT FILING DATE: 2004-01-30
  PRIOR APPLICATION NUMBER: US 60/308,958
  PRIOR FILING DATE: 2001-07-31
  PRIOR APPLICATION NUMBER: US 60/345,846
  PRIOR FILING DATE: 2001-11-09
  NUMBER OF SEQ ID NOS: 100
  SEQ ID NO 8
  LENGTH: 1048
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-485-225-8

SOFTWARE: FastSEQ for Windows Version 4.0

Query Match     88.2%;  Score 5483;  DB 34;  Length 1048;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1048;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTD 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MPVQAAQWTEFLSCPICYNEFDENVHKPISLGCSHTVCKTCLNKLHRKACPFDQTAINTD 60

Qy   61 IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVAS 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 IDVLPVNFALLQLVGAQVPDHQSIKLSNLGENKHYEVAKKCVEDLALYLKPLSGGKGVAS 120

Qy  121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANL 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 LNQSALSRPMQRKLVTLVNCQLVEEEGRVRAMRAARSLGERTVTELILQHQNPQQLSANL 180

Qy  181 WAAVARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 WAAVARGCQFLGPAMQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIG 240

Qy  241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 HVVQLLYRASCFKVTKRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQW 300

Qy  301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SSLLYGDLAHKSHMQSIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANI 360

Qy  361 DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLR 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 DPNPDAVSPTWEQLENAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLR 420

Qy  421 QQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTAGNVISVI 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 QQGGCPRGTNCTFAHSQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTAGNVISVI 480

Qy  481 GSTETTGKIVPSTNGISNAENSVSQLLSRSTDSTLRALETVKKVGKYGANGQNAAGPSAD 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GSTETTGKIVPSTNGISNAENSVSQLLSRSTDSTLRALETVKKVGKYGANGQNAAGPSAD 540

Qy  541 SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPPHSENIQYFQ 600
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 SVTENKIGSPPKTPVSNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPPHSENIQYFQ 600

Qy  601 DPRTQIPFEVPQYPQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 DPRTQIPFEVPQYPQTGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYST 660

Qy  661 FSPRDRMNSSPYQPPPPPQPYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 FSPRDRMNSSPYQPPPPPQPYGPVPPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPM 720

Qy  721 DVMHSSVYQTSLRERYNSLDGYYSVACQPPSERTTVLPLPREPCGHLKTSCEEQIRRKPD 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 DVMHSSVYQTSLRERYNSLDGYYSVACQPPSERTTVLPLPREPCGHLKTSCEEQIRRKPD 780

Qy  781 QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS 840
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 QWAQYHTQKAPLVSSTLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWS 840

Qy  841 CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP 900
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 CGTIGSCINAIDSEPKDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGP 900

Qy  901 IISKWGAISRSSRTGYHTTDPVQATASQGSSATKPISVSDYVPYVNAVDSRWSSSYGNEATS 960
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 IISKWGAISRSSRTGYHTTDPVQATASQGSSATKPISVSDYVPYVNAVDSRWSSSYGNEATS 960

Qy  961 SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE 1020
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 SAHYVERDRFIVTDLSGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDE 1020

Qy 1021 GRHLTLNLLSKEIELRNGELQSDYTEDA 1048
        ||||||||||||||||||||||||||||
Db 1021 GRHLTLNLLSKEIELRNGELQSDYTEDA 1048
```

```
RESULT 15
US-09-488-725A-3499
Sequence 3499, Application US/09488725A
GENERAL INFORMATION:
  APPLICANT: Hyseq Inc
  TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
  FILE REFERENCE: 784FLPCT
  CURRENT APPLICATION NUMBER: US/09/488,725A
  CURRENT FILING DATE: 2000-12-22
  PRIOR APPLICATION NUMBER: US/09/488,725
  PRIOR FILING DATE: 2000-01-21
  PRIOR APPLICATION NUMBER: US09/552,317
  PRIOR FILING DATE: 2000-04-25
  PRIOR APPLICATION NUMBER: US09/598,042
  PRIOR FILING DATE: 2000-06-20
  PRIOR APPLICATION NUMBER: US09/620,312
  PRIOR FILING DATE: 2000-07-19
  PRIOR APPLICATION NUMBER: US09/653,450
  PRIOR FILING DATE: 2000-08-31
  PRIOR APPLICATION NUMBER: US09/662,191
  PRIOR FILING DATE: 2000-09-14
  PRIOR APPLICATION NUMBER: US09/693,036
  PRIOR FILING DATE: 2000-10-19
  PRIOR APPLICATION NUMBER: US09/727,344
  PRIOR FILING DATE: 2000-11-29
  NUMBER OF SEQ ID NOS: 7144
  SOFTWARE: pt_FL_genes_b Versions 1.0
  SEQ ID NO 3499
  LENGTH: 870
  TYPE: PRT
  ORGANISM: Homo sapiens
US-09-488-725A-3499

Query Match     71.1%;  Score 4416;  DB 24;  Length 869;
Best Local Similarity    99.8%;  Pred. No. 0;
Matches 844;  Conservative   2;  Mismatches   0;  Indels   0;  Gaps   0;

Qy  196 MQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQLLYRASCFKVT 255
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MQEEALKLVLLALEDGSALSRKVLVLFVVQRLEPRFPQASKTSIGHVVQLLYRASCFKVT 60

Qy  256 KRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLAHKSHMQ 315
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 KRDEDSSLMQLKEEFRSYEALRREHDAQIVHIAMEAGLRISPEQWSSLLYGDLAHKSHMQ 120

Qy  316 SIIDKLQSPESFAKSVQELTIVLQRTGDPANLNRLRPHLELLANIDPNDAVSPTWEQLE 375
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Db    121 SIIDKLQSPESPAKSVQELTIVLQRTGDPANLNRLRPHLELLANIDPNPDAVSPTWEQLE 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    376 NAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLRQQGCPRGTNCTFAH 435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 NAMVAVKTVVHGLVDFIQNYSRKGHETPQPQPNSKYKTSMCRDLRQQGCPRGTNCTFAH 240

Qy    436 SQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISVIGSTETTGKIVPSTNG 495
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 SQEELEKYRLRNKKINATVRTFPLLNKVGVNNTVTTTAGNVISVIGSTETTGKIVPSTNG 300

Qy    496 ISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSADSVTENK1GSPPKTPV 555
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ISNAENSVSQLISRSTDSTLRALETVKKVGKVGANGQNAAGPSADSVTENK1GSPPKTPV 360

Qy    556 SNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPHSENIQYFQDPRTQIPFEVPQYPQ 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 SNVAATSAGPSNVGTELNSVPQKSSPFLTRVPVYPHSENIQYFQDPRTQIPFEVPQYPQ 420

Qy    616 TGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYSTFESPRDRMNSSPYQPP 675
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGYYPPPTVPAGVAPCVPRFVRSNNVPESSLPPASMPYADHYSTFESPRDRMNSSPYQPP 480

Qy    676 PPQPYGPVPVPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQTSLRER 735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 PPQPYGPVPVPVPSGMYAPVYDSRRIWRPPMYQRDDIIRSNSLPPMDVMHSSVYQTSLRER 540

Qy    736 YNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPDQWAQYHTQKAPLVSS 795
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 YNSLDGYYSVACQPPSEPRTTVPLPREPCGHLKTSCEEQIRRKPDQWAQYHTQKAPLVSS 600

Qy    796 TLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSCINAIDSEP 855
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TLPVATQSPTPPSPLFSVDFRADFSESVSGTKFEEDHLSHYSPWSCGTIGSCINAIDSEP 660

Qy    856 KDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGPIISKWGAISRSSRTG 915
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 KDVIANSNAVLMDLDSGDVKRRVHLFETQRRTKEEDPIIPFSDGPIISKWGAISRSSRTG 720

Qy    916 YHTTDPVQATASQGSATKPISVSDYVPVVNAVDSRWSSYGNEATSSAHYVERDRFIVTDL 975
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 YHTTDPVQATASQGSATKPISVSDYVPVVNAVDSRWSSYGNEATSSAHYVERDRFIVTDL 780

Qy    976 SGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDEGRHLTLNLLSKEIEL 1035
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 SGHRKHSSTGDLLSLELQQAKSNSLLLQREANALAMQQKWNSLDEGRHLTLNLLSKEIEL 840

Qy   1036 RNGELQ 1041
          ||||::
Db    841 RNGEVK 846
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